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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 01:11:00 ; Search time 6690 Seconds
(without alignments)

10748.511 Million cell updates/sec

Title: US-10-048-116-1

Perfect score: 1484

Sequence: 1 atgcggtgcagcagactct.....ttctccggactccgggtaa 1484

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484	100.0	1484	6	AX081280 Sequence
2	956.6	64.5	1446	6	BD137962 Monovalen
3	700.2	47.2	1045	6	CQ806515 Sequence
4	700.2	47.2	1108	6	CQ806531 Sequence
5	700.2	47.2	1108	6	CQ806532 Sequence
6	699.6	47.1	990	10	MMU294738
7	699.6	47.1	1095	10	MMUG66
8	699.6	47.1	1341	6	I07390 Sequence 4
9	699.6	47.1	1407	10	AF466698
10	699.6	47.1	1570	6	A22261 M.musculus
11	699.6	47.1	1570	6	AR029102 Sequence
12	699.6	47.1	1570	6	AR409372 Sequence
13	699.6	47.1	1570	6	AR559698 Sequence
14	699.6	47.1	1570	6	BD057272 Gene enco
15	699.6	47.1	1570	10	AB097847 Mus muscu
16	699	47.1	1158	6	AR160140 Sequence
17	699	47.1	1188	6	AR160149 Sequence
18	699	47.1	6729	6	AX080954 Sequence
19	699	47.1	7528	6	AX080953 Sequence

20	698	47.0	1581	6	A78881
21	698	47.0	1581	10	MMIGHC2AA
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23	697.4	47.0	1194	6	BD022360 Multi-fun
24	696.4	46.9	699	6	BD240891 Expressio
25	696.4	46.9	699	6	BD269243 Expressio
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27	695.4	46.9	1278	6	AR393789 Sequence
28	695.4	46.9	1278	6	AX084107 Sequence
29	695.4	46.9	2709	6	AR393797 Sequence
30	695.4	46.9	2709	6	AX084115 Sequence
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35	691.6	46.6	1584	10	BC003878 Mus muscu
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38	691.6	46.6	1639	10	BC080671 Mus muscu
39	691.6	46.6	1658	10	BC031470 Mus muscu
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ALIGNMENTS

RESULT 1
LOCUS AX081280 1484 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 1 from Patent WO0109194.
ACCESSION AX081280
VERSION AX081280.1 GI:13170129
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Glaichenhaus,N. and Malherbe,L.
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
JOURNAL Patent: WO 0109194-A 1 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
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/translations="MPCSRALILGVIALNTMLSLCGGDDIEDADHVGFGYGTVVQSPG DIQYTHFEDGDLFYDLDKKTVMRLPEFGQLILFEPQGLQNTAAEKNLGLTK RSNFTATNEAQPATVPKSPVLLGWPNTLFCVDNIFPVPVINTLWRNKSVDGVY ETSFLVNRDHSFKLSVLTPIPSDDDIYDCKVEHMGLEEPVLKHWEPEIAPMSELTE TGGGSGTAPSAQLEKELQALENAQLELQALEKELQAASERPPTIKPCPCK CPAPNLLGGPSVTFPPKIKDVLMSISLPVTCVVVDSEDDPQVLSFWFNNVEVHT AQOTFHREDYNSLTVVVSALPIHQDMWSGKFKCNNDKLPAPILBERTISKPKGSVR APQVYVLPPEEEMTKQVLTCTMTDFMPEDIYVEWTNNGKTELNTKNTPEVLDSVG SYFMYSKLRVEKKMWNVERNSYSCSVVHGLEHNNHTTKSFSRTPC"

ORIGIN

Query Match 100.0%; Score 1484; DB 6; Length 1484;
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Matches 1484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy 176 TCTATGTGGACTTGGATAAGAAACCTGCTCGAGGCTTCCTGAGTTTGGCCAAATTGA 235
Db 110 TCCATGTGGATATGCAAGAGAGAGCGGTCTGGCGGCTTGAAGATTTGGACGATTTG 169

Qy 236 TACTCTTTGAGCCCAAGGTGGAATGCAAAACATAGCTGCAAAAAACAACTTTGGAA 295
Db 170 CCAGCTTTGAGGCTCAAGGTGCAATGGCCAAACATAGCTGTGGACAAAAGCCAACTTGGAAA 229

Qy 296 TCTTGACTTAGAGCTCAAAATTTACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
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Db 290 TCAGCAACAGCCCTGTGGAATGAGAGGCGCAAGCTCCTCATCTGTTTCATAGCAAGT 349

Qy 416 TCTTCCCACTGTGATCAACATCATGCTGCTCAGAAATAGCAAGTCAAGTCAAGCGCG 475
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Qy 476 TTTATGAGACAGCTTCTCTGCTCAACCGTGACCATCTCTTCCACAGCTGCTTATCTCA 535
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Qy 536 CTTTCATCTCTCTGATGATCACAATTTATGACTCAAGGTGGAGCACTGGGGCTGGAGG 595
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Db 590 TCGACGGAGGTGGCGGGTTTAACTGATACATCTCAAGCGGAGACAGATCAACTTGAAG 649

Qy 701 AAGAGCTCCAGGCCCTGGAGAGGAATGACACAGCTGGAATGGAGTTGCAAGCACTGG 760
Db 650 ACGAAGATCTGCGTTGCAAGCCGAGATGCGCAATCTACTGAAGAGAGGAAGAACTGG 709

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Qy 938 ATGTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACTGGAAGTAC 997
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1478 CGGGTAA 1484
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RESULT 3
Q806515
LOCUS Q806515 1045 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 10 from Patent WO2004035622.
ACCESSION Q806515
VERSION Q806515.1 GI:47111911
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dreher, I. and Moll, T.
TITLES Antagonists 11-15
JOURNAL Patent: WO 2004035622-A 10 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..1045
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/db_xref="taxon:32630"
/notes="DNA for fusionprotein"

ORIGIN
Query Match 47.2%; Score 700.2; DB 6; Length 1045;
Best Local Similarity 93.2%; Pred. No. 5.5e-181;
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 700 AAAGAGCTCCAGGCCCTGGAGAGGAAGAAATGACAGCTGGAATGGGAGTTGCCAAGCACTG 759
Db 256 AAAGATGTGAGGAACTGGAGGAAAGAAATATTAAGAAATTTTGCAGAGTTTGTACAT 315

Qy 760 GAAAGAGAACTGGCTCAGGAGCATCTGAGCCAGAGGGCCCCCAATCAAGCCCTGTCT 819
Db 316 ATGTCTCCAAATGTTTCATCAACACTTCGGATCCAGAGGGCCCCCAATCAAGCCCTGTCT 375

Qy 820 CCATGCAAAATGCCAGACCTTAACCTCTTGGGTGGACCATCCGCTTTCATCTTCCCTCCA 879
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Query Match      47.2%; Score 700.2; DB 6; Length 1108;
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Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy 319 AAAGATGTGAGGAAGTGGAGGAAATATTAAGAAATTTTGGACAGTTTGTATCAT 378
Db 319 |||||
Qy 760 GAAAAGGAACCTGGCTAGCGAGCATCTGAGCGCCAGAGGGCCCAATCAAGCCCTGTCT 819
Db 760 |||||
Qy 379 ATTGTCCAAATGTTTCATCAACACTTCGGATCCAGAGGGCCCAATCAAGCCCTGTCT 438
Db 379 |||||
Qy 820 CCATGCAATGCCAGACACTAACTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 879
Db 820 |||||
Qy 439 CCATGCAATGCCAGCACTTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA 498
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Qy 880 AAGATCAAGGATGTACTCATCATCTCTCCAGAGCCCATAGTCACATGTGTGGTGGAT 939
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Qy 499 AAGATCAAGGATGTACTCATCATCTCTCCAGAGCCCATAGTCACATGTGTGGTGGAT 558
Db 499 |||||
Qy 940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTTTGTGAACAACTGGAAGTACAC 999
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Qy 559 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTTTGTGAACAACTGGAAGTACAC 618
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Qy 1000 ACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCAAGTCC 1059
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Qy 1480 GGTAA 1484
Db 1099 GGTAA 1103

RESULT 6
MMU294738
LOCUS MMU294738 990 bp mRNA linear ROD 09-FEB-2001
DEFINITION Mus musculus partial mRNA for immunoglobulin heavy chain constant region gamma2a (IGHG2A gene).
ACCESSION AJ294738
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Db	642	TGAGCCAGAGGGCCCAATCAAGCCCTGCTCCATGCAAAATGCCAGCACCTAAACCT	701
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Qy	906	CCTGAGCCCATAGTACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGCCA	965
Db	762	CCTGAGCCCATAGTACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGCCA	821
Qy	966	GATCAGCTGGTTCGTGAACAGTGGAGTACACACAGCTCAGACACAAACCCATAGAGA	1025
Db	822	GATCAGCTGGTTCGTGAACAGTGGAGTACACACAGCTCAGACACAAACCCATAGAGA	881
Qy	1026	GGATTACAAAGTACTCTCCGGGTGGTCAAGTCCCTCCCAATCCAGACACAGGACTGGAT	1085
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Qy	1086	GAGTGGCAAGAGTTCAAATGCAAGGTCAACAAAGAGCTCCAGCGCCCATCGAGAG	1145
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Qy	1206	AGAAAGAGAGTACTTAAGAAACAGGTCACTCTGACCTGCATGTGTCAAGACTTTCATGCC	1265
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Qy	1266	TGAAGACATTTACGTGGAGTGGACCAACAAACCGGAAACAGAGCTTAACTACAAGAACAC	1325
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Qy	1386	GAAGAACTGGGTGGAAAGAAATAGTACTCTGTTTCAAGTGGTCCAGAGGCTTGCACAA	1445
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Qy	1446	TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA	1484
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RESULT 9
AF466698
LOCUS
DEFINITION Mus musculus strain BALB/c immunoglobulin heavy chain mRNA, partial cds.
ACCESSION AF466698
VERSION AF466698.1 GI:27127159
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1407)
Lai, Y.-S., John, J.A.C., Guo, I.-C., Chen, S.-C., Fang, K. and Chang, C.-Y.
In vitro efficiency of intra- and extracellular immunization with mouse anti-YGNV antibody against yellow grouper nervous necrosis virus
JOURNAL Vaccine 20 (25-26), 3221-3229 (2002)
MEDLINE 22154004
PUBMED 12163274
REFERENCE 2 (bases 1 to 1407)
Lai, Y.-S., John, J.A.C., Guo, I.-C., Chen, S.-C., Fang, K. and Chang, C.-Y.
Direct Submission
TITLE Submitted (08-JAN-2002) Institute of Zoology, Academia Sinica, 128 Academia Road, Nankang, Taipei 11529, Taiwan, ROC

FEATURES
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Query Match	47.1%;	Score 699.6;	DB 10;	Length 1407;
Best Local Similarity	100.0%;	Pred. No. 8.3e-181;		
Matches 699;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	1386	GAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTCAGTGGTCCACGAGGGTCTGCACAA	1445	
Db	1308	GAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTCAGTGGTCCACGAGGGTCTGCACAA	1367	
Qy	1446	TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA	1484	
Db	1368	TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA	1406	

RESULT 10
A22261
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
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AUTHORS
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JOURNAL
FEATURES
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DEFINITION Sequence 6 from patent US 6632927.
ACCESSION AR409372
VERSION AR409372.1 GI:40160268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 1570)
Unclassified.

AUTHORS Adair,J.R., Athwal,D.S. and Emtage,J.S.
TITLE Humanized antibodies

JOURNAL Patent: US 6632927-A 6 14-OCT-2003;
FEATURES Location/Qualifiers

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LOCUS AR559698 1570 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 6 from patent US 6750325.
ACCESSION AR559698
VERSION AR559698.1 GI:53969764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 1570)
Unclassified.

AUTHORS Jolliffe,J.K., Zivin,R.A., Adair,J.R. and Athwal,D.S.
TITLE CD3 specific recombinant antibody

JOURNAL Patent: US 6750325-A 6 15-JUN-2004;
FEATURES Location/Qualifiers

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DEFINITION Gene encoding antimalathion monoclonal antibody.
ACCESSION BD057272
VERSION BD057272.1 GI:22602878
KEYWORDS JP 2001275682-A/9,
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1570)
AUTHORS Okawa,H., Nakata,M. and Yuasa,Y.
TITLE Gene encoding antimalathion monoclonal antibody
JOURNAL Patent: JP 2001275682-A 9 09-OCT-2001;
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PD 09-OCT-2001
PF 31-MAR-2000 JP 2000098323
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AB097847
ACCESSION AB097847
VERSION AB097847.1 GI:26665399
SOURCE Mus musculus (house mouse)
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REFERENCE 1 Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K., Kawata,M. and Ohkawa,H. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Molecular characteristics of the monoclonal and recombinant antibodies specific to the insecticide malathion
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1570)
AUTHORS Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K., Kawata,M. and Ohkawa,H. Direct Submission
JOURNAL Submitted (11-DEC-2002) Kosuke Nishi, Kobe University, Research Center for Environmental Genomics, 1-1 Rokkodai-cho, Nada-ku, Kobe, Hyogo 651-8501, Japan (E-mail:nishikosuke@yahoo.co.jp, Tel:81-78-803-5863, Fax:81-78-871-3617)
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Best Local Similarity 100.0%; Pred. No. 8.4e-181;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Post-processing: Minimum Match 0%
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8	700.2	47.2	1108	12	Ado07578 Fusion pr
9	699.2	47.2	1108	12	Ado07577 Fusion pr
10	699.6	47.1	990	12	Adl15694 Murine im
11	699.6	47.1	1570	2	AAQ12637 Monoclonal
12	699.6	47.1	1570	12	Adq91058 Murine OK
13	699.2	47.1	729	3	Aaz35704 Human gly
14	699.2	47.1	1140	10	AdE85817 Murine in
15	699	47.1	1158	2	AAT59350 1-153 del
16	699	47.1	1188	2	AAT59349 1-153 c-m
17	699	47.1	6729	4	AAF30341 Bicistron
18	699	47.1	7528	4	AAF30316 Bicistron
19	698	47.0	1341	1	AAN91659 Chimeric
20	698	47.0	1581	2	AAQ48037 Monoclonal

21	698	47.0	1645	2	AAQ54652 T84.12 He
22	697.4	47.0	1131	2	AAV55416 Chimeric
23	697.4	47.0	1194	2	AAV55415 Chimeric
24	697.4	47.0	1275	2	AAT62850 Mouee sol
25	696.4	46.9	699	3	Aaz51300 Murine im
26	696.4	46.9	699	3	AAAS0055 Mousee imm
27	696.4	46.9	1707	3	AAZ35706 Human gly
28	696.2	46.9	1140	10	ADBE5819 Murine mu
29	695.4	46.9	1278	4	AAF76881 DNA encod
30	695.4	46.9	2709	4	AAF76889 Coding se
31	695	46.8	700	12	Ado07569 Fusion pr
32	693.2	46.7	1356	12	Adn97544 Artificia
33	693.2	46.7	1461	6	Adad22972 Mousee zal
34	689.2	46.4	10512	4	AAAD09085 PUB115 pl
35	689.2	46.4	10512	6	AAK99698 DNA of pl
36	688.4	46.4	702	4	AAAD09045 Murine Im
37	688.4	46.4	702	6	AAK99695 Mousee Igg
38	687.4	46.3	777	12	ADQ31223 Cla88 II
39	682.8	46.0	1146	12	Adi01041 Human/mur
40	681.6	45.9	1098	9	ACC43452 Nucleotid
41	681	45.9	1209	2	AAx34597 Murine IL
42	656.4	44.2	4713	2	AAV12067 Murine IA
43	650.4	43.8	2053	4	ABi99029 IAS MBP 9
44	650.4	43.8	2059	4	ABi99032 MBP 1-14
45	608.4	41.0	776	2	AAQ03169 Sequence

ALIGNMENTS

RESULT 1
AAF55098
ID AAF55098 standard; DNA; 1484 BP.

XX AAF55098;

AC AAF55098;

XX 15-MAY-2001 (first entry)

XX DNA encoding a fusion protein comprising an alpha chain of MHC.

XX Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;

XX major histocompatibility complex; PC region; antigen; T lymphocyte;

XX immunostimulant; vaccine; infection; tumour; ss.

XX Synthetic.

XX Key Location/Qualifiers

PH CDS i..1482

FT /*tag= a

XX WO200109194-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-FR002193.

XX 29-JUL-1999; 99FR-00009862.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Glaichenhaus N, Malherbe L;

XX WPI; 2001-182944/18.

XX P-PSDB; AAB67480.

XX New soluble recombinant protein, useful e.g. as immunostimulant,

XX comprises dimeric major histocompatibility complex molecule fused to

XX immunoglobulin Fc region.

XX Example 1; Page 31-33; 43pp; French.

XX The specification describes soluble recombinant proteins that comprise at

CC least a dimer formed from the alpha and beta-chains of MHC (major

CC histocompatibility complex) Class I and II molecules in which at least
CC one chain has, attached to its C-terminus, at least part of the Fc region
CC of an immunoglobulin. The recombinant proteins, when linked to an
CC antigenic peptide, are used to count and/or purify antigen-reactive T
CC lymphocytes and to characterize their phenotype, e.g. in preclinical
CC evaluation of vaccines. They are also used as immunostimulants,
CC particularly for vaccine development (against infections and tumours), to
CC count and determine phenotype of autoreactive T cells in subjects with,
CC or at risk of developing, autoimmune diseases, e.g. for staging or
CC evaluating treatments, and (to purify and/or enrich Ag-reactive T cells
CC from cell cultures or patient samples, for use in subsequent curative or
CC preventative cellular therapy. The present sequence encodes a recombinant
CC protein of the invention, comprising an alpha chain of MHC molecules
XX

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1484;	DB 5;	Length 1484;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1484;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGCGGTGAGAGAGAGCTGTAATCTGGGGTCTCGCCCTGGAACACATGCTAGCCTC 60
Db 1 ATGCGGTGAGAGAGAGCTGTAATCTGGGGTCTCGCCCTGGAACACATGCTAGCCTC 60
QY 61 TCGCGAGGTGAAG 120
Db 61 TCGCGAGGTGAAG 120
QY 121 CAGTCTCTGGAG 180
Db 121 CAGTCTCTGGAG 180
QY 181 GTGAGCTTGGAG 240
Db 181 GTGAGCTTGGAG 240
QY 241 TTTGAGCCCCAGGTGGAG 300
Db 241 TTTGAGCCCCAGGTGGAG 300
QY 301 ACTAAGAGGTCAAATTTACCCCGAGTACCAATGAGGCTCTCAAGCGAGCTGTGTCC 360
Db 301 ACTAAGAGGTCAAATTTACCCCGAGTACCAATGAGGCTCTCAAGCGAGCTGTGTCC 360
QY 361 AAGTCCCTGTGCTGTGGTTCAGCCCAACACCCCTTATCTGCTTTTGGAGAGAGAG 420
Db 361 AAGTCCCTGTGCTGTGGTTCAGCCCAACACCCCTTATCTGCTTTTGGAGAGAGAG 420
QY 421 CCACCTGTGATCAACATCACATGAGTCAAGATAGCAATGAGTCAAGAGAGAGAGAG 480
Db 421 CCACCTGTGATCAACATCACATGAGTCAAGATAGCAATGAGTCAAGAGAGAGAGAG 480
QY 481 GAGACAGCTTCTCGTCAACCGTGACCAATCTCTTCCACAGCTGTCTTATCTACCTTC 540
Db 481 GAGACAGCTTCTCGTCAACCGTGACCAATCTCTTCCACAGCTGTCTTATCTACCTTC 540
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCG 600
Db 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCG 600
QY 601 GTTCTGAAACATCTGGAG 660
Db 601 GTTCTGAAACATCTGGAG 660
QY 661 GTTCTGAAACATCTGGAG 720
Db 661 GTTCTGAAACATCTGGAG 720
QY 721 AAGGAG 780
Db 721 AAGGAG 780
QY 781 GCATCTGAGCCAG 840

Db	781	GCATCTGAGCCAG	840
QY	841	AACCTCTGGGTGAG	900
Db	841	AACCTCTGGGTGAG	900
QY	901	ATCTCCCTGAGCCAG	960
Db	901	ATCTCCCTGAGCCAG	960
QY	961	GTCCAGATCAGCTGCTGTTTGTGAACAACAGTGGAGTACACACAGCTCAGACAAACCCAT	1020
Db	961	GTCCAGATCAGCTGCTGTTTGTGAACAACAGTGGAGTACACACAGCTCAGACAAACCCAT	1020
QY	1021	AGAGAGAGATTACACAGTACTCTCCGGGTGGTTCAGTGGCTCCCTCCCATCCAGCAGGAC	1080
Db	1021	AGAGAGAGATTACACAGTACTCTCCGGGTGGTTCAGTGGCTCCCTCCCATCCAGCAGGAC	1080
QY	1081	TGGATGAGTGGCAAGGAGTTCAAAATGCAAGTCAACAAAGACCTCCAGCCGCCATC	1140
Db	1081	TGGATGAGTGGCAAGGAGTTCAAAATGCAAGTCAACAAAGACCTCCAGCCGCCATC	1140
QY	1141	GAGAGAAACCATCTCCAAACCCAAAGAGTCAAGTAAAGAGTCCACAGGTATATGTCTTGCCT	1200
Db	1141	GAGAGAAACCATCTCCAAACCCAAAGAGTCAAGTAAAGAGTCCACAGGTATATGTCTTGCCT	1200
QY	1201	CCACAG	1260
Db	1201	CCACAG	1260
QY	1261	ATGCTGAG	1320
Db	1261	ATGCTGAG	1320
QY	1321	AACACTGAACAGTCTCGGAGTCTGATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1380
Db	1321	AACACTGAACAGTCTCGGAGTCTGATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1380
QY	1381	GAAGAAG	1440
Db	1381	GAAGAAG	1440
QY	1441	CACATCACCACAG	1484
Db	1441	CACATCACCACAG	1484

RESULT 2

ABI99041
ID ABI99041 standard; cDNA; 1676 BP.

XX AC ABI99041;

XX DT 25-FEB-2002 (first entry)

XX DE Murine pCB223 coding sequence.

XX KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
XX single chain; immunosuppressive; antidiabetic; antiinflammatory;
XX antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
XX autoimmune disease; insulin dependent diabetes; multiple sclerosis;
XX myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
XX rheumatoid arthritis; systemic lupus erythematosus; ss.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO200170245-A1.

XX PD 27-SEP-2001.

XX PF 22-MAR-2001; 2001WO-US0099616.

XX 22-MAR-2000; 2000US-0191274P.
PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX (CORI-) CORIXA CORP.
XX
XX Carter D, Zhu S, Arimilli S, Wang A;
XX WPI; 2001-616371/71.
XX P-PSDB; ABB56471.
XX
PT Multimeric complex for treating autoimmune diseases, comprises first and
PT second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
XX Disclosure; Page 115; 147pp; English.
XX
CC The invention relates to a multimeric complex comprising a first
CC recombinant single chain major histocompatibility complex (MHC) class II
CC molecule and a second recombinant single chain MHC class II molecule,
CC each comprising an alpha1 domain and a beta1 domain linked through an
CC amino acid linker and a multimerization domain. The first and the second
CC molecule are linked through the multimerization domain to form a
CC multimeric complex. The complex is useful for treating autoimmune
CC diseases. It is useful for treating insulin dependent diabetes, multiple
CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
CC erythematosus. The present sequence encodes a single chain MHC class II
CC molecule of the invention
XX
SQ Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

Query Match 71.9%; Score 1066.4; DB 4; Length 1676;
Best Local Similarity 83.5%; Pred. No. 4.4e-277;
Matches 1318; Conservative 0; Mismatches 96; Indels 164; Gaps 3;

QY 67 GGTGAAGACGACATTGAGGCGGACGAGTGGCTTCTATGGTACAACTGTTTATCAGTCT 126
DB 91 GGCAGACGACATTGAGGCGGACGAGTGGCTTCTATGGTACAACTGTTTATCAGTCT 150

QY 127 CTTGGAGACATTGGCCAGTACACATGAAATTTGATGGTGAATGATGTTCTATGTTGAC 186
DB 151 CTTGGAGACATTGGCCAGTACACATGAAATTTGATGGTGAATGATGTTCTATGTTGAC 210

QY 187 TTGATGAAGAGAACTGTTGAGGCTTCTGAGGCTTCTGAGTTCGCAATTTGATGACTTTT 246
DB 211 TTGATGAAGAGAGACTATCTGGATGCTTCTGAGTTCGCAATTTGATGACTTTT 270

QY 247 CCCCAAGGTGACATGCAAAACATAGCTGCAGAAAACACAACTTGGGAATCTTGACTAAG 306
DB 271 CCCCAAGGTGACATGCAAAACATAGCTGCAGAAAACATAGCTTGGGAATCTTGACTAAG 330

QY 307 AGGTCAAATTTCAACCCAGCTACCAATGAGGCTTCTCAAGGAGCTGTTTCCCAAGTCC 366
DB 331 AGGTCAAATTTCAACCCAGCTACCAATGAGGCTTCTCAAGGAGCTGTTTCCCAAGTCC 390

QY 367 CTTGTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTTGGCAACATCTTCCCACT 426
DB 391 CTTGTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTTGGCAACATCTTCCCACT 450

QY 427 GTGATCAACATCATATGGCTCAGAAATAGCAAGTCAAGTCAAGCGCGGTTTATGAGACC 486
DB 451 GTGATCAACATCATATGGCTCAGAAATAGTATGATCAAGCGCGGTTTATGAGACC 510

QY 487 AGCTTCTCTGTCACCGTACCAATTTCTTCCCAAGCTGTTTATCTCACTTCACTCCCT 546
DB 511 AGCTTCTCTGTCACCGTACCAATTTCTTCCCAAGCTGTTTATCTCACTTCACTCCCT 570

QY 547 TCTGATGATCACTTTATGATGCAAGTGTGAGCACTGGGGCTTGGAGGAGCGGTTCTG 606
DB 571 TCTGATGATGATTTTATGATGCAAGTGTGAGCACTGGGGCTTGGAGGAGCGGTTCTG 630

QY 607 AAACACTGGGAACCTGAGATTTCAGAGCCCCCATGTCAGAGCTGACAGAAACTGGAGGTGA 666
DB 631 AAACACTGGGAACCTGAGATTTCAGAGCCCCCATGTCAGAGGATCTGCCAAAACACAGCC 690

QY 667 GGAT----- 670
DB 691 CCATCGGTCTATCCATGGCCCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTA 750
QY 671 ----- 670
DB 751 GGATCGCTGTCAGGGGTATTTCCTTGAGCCAGTGGACCTTGGAACTCTGGATCC 810

QY 671 ----- 686
DB 811 CTGTCCAGTGTGTGCACACCTTCCAGCTGTCTCTGAGTCTGACCTCTACACCTCAGC 870

QY 687 AGCTCAGCTGAAAAGAGCTCCAGGCCCTTGAGAGAGAAAATGACAGCTGGAAATGGGA 746
DB 871 AGCTCAG--TGACTGTAACTCTGAGCACCTTGGGCCAGCCAGTCCATCCTGCAATGGG 928

QY 747 GTTGAAGCACTGMAAAGAACTGGCTCAGGCGAGCATCTGAGCCAGAGGGCCCACAAT 806
DB 929 CCACCCGCGAGCAGCACCAGGTGACAAAGAA--AATTGAGCCCAAGAGGCCCAACAT 986

QY 807 CAAGCCCTGTCTCCATGCAAAATGCCAGCACCTTAACCTCTTGGGTGGACCATCCGCTTT 866
DB 987 CAAGCCCTGTCTCCATGCAAAATGCCAGCACCTTAACCTCTTGGGTGGACCATCCGCTTT 1046

QY 867 CATCTTCCCTCAAAGATCAAGGATGTACTCATGATCTCCTGAGGCCCATAGTCAATG 926
DB 1047 CATCTTCCCTCAAAGATCAAGGATGTACTCATGATCTCCTGAGGCCCATAGTCAATG 1106

QY 927 TGTGTTGGTGTGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTTTGTGAACA 986
DB 1107 TGTGTTGGTGTGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTTTGTGAACA 1166

QY 987 CGTGAAGATACACAGCTCAGACACAAACCCATAGAGAGATTTACAACTACTCTCCG 1046
DB 1167 CGTGAAGATACACAGCTCAGACACAAACCCATAGAGAGATTTACAACTACTCTCCG 1226

QY 1047 GGTGTTGAGTGCCTTCCCATCAGACACAGGACTGATGAGTGGCAAGGATTTCAATG 1106
DB 1227 GGTGTTGAGTGCCTTCCCATCAGACACAGGACTGATGAGTGGCAAGGATTTCAATG 1286

QY 1107 CAAGTCAACAAACAGAGCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1166
DB 1287 CAAGTCAACAAACAGAGCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1346

QY 1167 GTCAAGTAAAGCTCCAGATATATGTTTGGCTTCCACCAAGAGAGAGATGACTAAGAA 1226
DB 1347 GTCAAGTAAAGCTCCAGATATATGTTTGGCTTCCACCAAGAGAGAGATGACTAAGAA 1406

QY 1227 ACAGGTCACTCTGACCTGATGTCAGATCTTATGCTTCCATGCTGAAAGCAATTTACGTTGAGTG 1286
DB 1407 ACAGGTCACTCTGACCTGATGTCAGATCTTATGCTTCCATGCTGAAAGCAATTTACGTTGAGTG 1466

QY 1287 GACCAACACGGGAAACAGAGCTAACTACAGAACACCTGAAACCACTGCTGGACTCTGA 1346
DB 1467 GACCAACACGGGAAACAGAGCTAACTACAGAACACCTGAAACCACTGCTGGACTCTGA 1526

QY 1347 TGTCTTCTTACTTCACTGATGACAGCAAGTGTGAGTGGAAAAGAACTGGGTGGAAAGAAA 1406
DB 1527 TGTCTTCTTACTTCACTGATGACAGCAAGTGTGAGTGGAAAAGAACTGGGTGGAAAGAAA 1586

QY 1407 TAGCTACTCTCTGTTAGTGTGTCCAGGGTGTGTGCAAAATCAACCAACGACTAAGAGCTT 1466
DB 1587 TAGCTACTCTCTGTTAGTGTGTCCAGGGTGTGTGCAAAATCAACCAACGACTAAGAGCTT 1646

QY 1467 CTCCCGGACTCCGGGTAA 1484
DB 1647 CTCCCGGACTCCGGGTAA 1664

RESULT 3	
AAT99707	
ID	AAT99707 standard; cDNA; 1446 BP.
XX	
AC	AAT99707;
DT	17-OCT-2003 (revised)
DT	17-AUG-1998 (first entry)
XX	
DE	DR2-IgG fusion construct.
XX	
KW	Major histocompatibility complex class II; MHC class II; human; mouse;
KW	fusion protein; HLA-DR2; DR2*0101; binding domain; Fos;
KW	dimerisation domain; IGG; allergy; autoimmune disease; vaccine;
KW	multiple sclerosis; therapy; ss.
XX	
OS	Homo sapiens.
OS	Mus musculus.
OS	Chimeric.
XX	
PN	WO9806749-A2.
XX	
PD	19-FEB-1998.
XX	
PF	15-AUG-1997; 97WO-US014503.
XX	
PR	16-AUG-1996; 96US-0024077P.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	Wucherpennig KW, Strominger JL;
XX	
DR	WPI; 1998-159459/14.
XX	
PT	New Class II MHC fusion proteins - comprising a MHC Class II binding
PT	domain and a dimerisation domain or an immunoglobulin region used for
PT	modulating immune responses.
XX	
PS	Example; Page 49; 76pp; English.
XX	
CC	This nucleotide sequences codes for a bivalent DR2 fusion protein
CC	obtained by fusion of the Fc portion of IgG2a to the 3' end of a DR-alpha
CC	-Fos cDNA construct (see AAV16966). The Fc portion was amplified by RT-
CC	PCR from mouse hybridoma L243. The PCR product was then fused in frame
CC	with the DR-alpha-Fos construct by overlapping PCR. The DR2-IgG fusion
CC	was expressed in the Drosophila Schneider cell system. The invention
CC	relates to new soluble monovalent and multivalent Class II MHC fusion
CC	proteins comprising a MHC Class II binding domain and a dimerisation
CC	domain or an immunoglobulin region that can be used for the treatment of
CC	allergic and autoimmune diseases (e.g. multiple sclerosis), for tissue
CC	tolerising a subject to foreign tissue before or after organ or tissue
CC	transplantation, or for vaccination against pathogens. (Updated on 17-OCT
CC	-2003 to standardise OS field)
XX	
SQ	Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;
Query Match	64.5%; Score 956.6; DB 2; Length 1446;
Best Local Similarity	81.8%; Pred. No. 1.8e-247;
Matches 1135; Conservative	0; Mismatches 234; Indels 18; Gaps 2;
QY	116 TTTATCAGTCTCCTCGAGACATTGGCCAGTACACACATGAATTTTCATGGTGTGATGTTGT 175
DB	50 TCTATCTGAATCCTGACCAATCAGCGGAGTTTATGTTTTCATGTTTTCATGGTGTGATGATTT 109
QY	176 TCTATGTGGACTTGGATAAGAGAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAAATTGA 235
DB	110 TCCATGTGGATATGCAAGAAGAGACGGTCTGCGGCTTGAAGATTTGGACGATTG 169
QY	236 TACTCTTTGAGCCCAAGGTGACATGCGAAACATAGCTGCGAGAAACACAACTTTGGAA 295
DB	170 CCAGCTTTTGAGGCTCAAGGTGCATTTGGCCAAACATAGCTGTGACAAAGCCAACTTTGAAA 229
QY	296 TCTTGACTAAGAGGTCAAATTTACCCCGAGCTACCAATGAGGCTCTCTCAAGGAGCTGTGT 355

Db	230	TCATGACAAAGCGCTCCAACTATACTCCGATCAACCAATGTACTCTCCAGAGTAACTGTGC	289
QY	356	TCCCAAGTCCCTGTGTGCTGTGGGTAGCCCAACACCTTATCTGTCTTTGTGGCAACA	415
Db	290	TCAGAAACAGCCCTGTGGAACTGAGAGAGCCCAACGCTCTCATCTGTTTCATAGACAA	349
QY	416	TCTTCCACCTGTGATCAACATCATCATGGCTCAGAAATAGCAAGTCACTCACAGACGG	475
Db	350	TCACCCCAACAGTGGTCAATGTCACTGGCTTCGAAATGGAATGGAATGGAATGGAATG	409
QY	476	TTTATGAGACAGCTTCTCTGTCACCTGACCAATTCCTCCACAAGCTGTCTTATCTCA	535
Db	410	TGTCAGAGACAGTCTTCTGCTCCAGGGAAGACCACTTTTCGGCAAGTTCACATATCTCC	469
QY	536	CTTTCATCCCTTGTGATGATCAATTTATGATGCAAGGTGGAGCACTGGGGCTGGAGG	595
Db	470	CTTTCCTGCCCTCAACTGAGGACGTTTACGACTGCAGGTTGAGCACTGGGGCTGGATG	529
QY	596	AGCCGGTTCTGAACACACTGGGAACTGAGATTCAGCCCCCATGTGTCAGAGCTGACAGAA	655
Db	530	AGCCTCTTCTCAAGCACTGGGAGTTTGATGTCCAAAGCCCTCTCCAGAGACTACAGAG	589
QY	656	CTGGAGGTGGAGGATCCACT-----ACAGCTCCATCAGCTCAGCTCGAAA	700
Db	590	TCGACGGAGGTGGCGGGTTTAACTGATACACTCCAAGCGGAGACAGATCAACTTGAAG	649
QY	701	AAGAGCTCCAGGCCCTGGAGAAAGAAATGACAGCTGGAATGGAGTTGCAAGCACTGG	760
Db	650	ACGAGAAGTCTGCGTTGACAGCCGAGATTGCCAATCTACTGAAGAGAAGAAACTGG	709
QY	761	AAAAGGAAGCTG---GCTCAGGACAGCTGTAGCCCCAGAGGGCCCCCAATCAAGCCCTGTC	817
Db	710	AGTTTCATCTCGCCGCCCATCGACATCTGAGCCAGAGGGCCCCCAATCAAGCCCTGTC	769
QY	818	CTCCATGCAAAATGCCAGCACTTAACCTCTTTGGGTGGACCACTCCGTCTTCACTTCCCTC	877
Db	770	CTCCATGCAAAATGCCAGCACTTAACCTCTTTGGGTGGACCACTCCGTCTTCACTTCCCTC	829
QY	878	CAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACTGTGTGGTGGTG	937
Db	830	CAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACTGTGTGGTGGTG	889
QY	938	ATGTGAGCGAGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACCTGGAGTAC	997
Db	890	ATGTGAGCGAGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACCTGGAGTAC	949
QY	998	ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCACTG	1057
Db	950	ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCACTG	1009
QY	1058	CCCTCCCATCCAGCACCAAGGAGTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACA	1117
Db	1010	CCCTCCCATCCAGCACCAAGGAGTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACA	1069
QY	1118	ACAAAGACTCCAGCGCCCATCGAGAGAACATCTCAAAACCCCAAGGGTCAAGTAAAG	1177
Db	1070	ACAAAGACTCCAGCGCCCATCGAGAGAACATCTCAAAACCCCAAGGGTCAAGTAAAG	1129
QY	1178	CTCCACAGGTATATGTCTTGTGCTCCACAGAAAGAGATGACTAAGAAACAGGTCACCTC	1237
Db	1130	CTCCACAGGTATATGTCTTGTGCTCCACAGAAAGAGATGACTAAGAAACAGGTCACCTC	1189
QY	1238	TGACCTGCATGGTCAAGACTTTCATGCTGAGACATTTTACGTGGAGTGGACCAACAG	1297
Db	1190	TGACCTGCATGGTCAAGACTTTCATGCTGAGACATTTTACGTGGAGTGGACCAACAG	1249
QY	1298	GGAAACAGAGCTAAACTAGAAACACTGAAACAGTCTCGACTCTGATGGTCTTACT	1357
Db	1250	GGAAACAGAGCTAAACTAGAAACACTGAAACAGTCTCGACTCTGATGGTCTTACT	1309
QY	1358	TCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCT	1417


```

Db 1310 TCATGTACAGCACTGAGAGTGGAAGAAGAAAGAACTGGGTGGAAGAAATAGTACTCCT 1369
Qy 1418 GTTCAGTGGTCCAGAGGGTCTGCACAATCACCACACAGACTTAAGAGCTTCTCCCGGACTC 1477
Db 1370 GTTCAGTGGTCCAGAGGGTCTGCACAATCACCACACAGACTTAAGAGCTTCTCCCGGACTC 1429
Qy 1478 CGGGTAA 1484
Db 1430 CGGGTAA 1436

RESULT 4
AAX87813
ID AAX87813 standard; DNA; 1446 BP.
XX
XX AAX87813;
AC
XX
XX 09-NOV-1999 (first entry)
XX
XX HLA-DR2 alpha-Fos-IgG fusion construct.
XX
XX Major histocompatibility complex Class II; MHC; binding domain; HLA-DR2;
XX leucine zipper; Fos; IgG; Fc; immunoglobulin; antibody; fusion protein;
XX multiple sclerosis; rheumatoid arthritis; graft rejection; allergy;
XX autoimmune disease; pemphigus vulgaris; systemic lupus erythematosus;
XX T lymphocyte; T cell; diagnosis; therapy; adoptive immunotherapy; ss.
XX
XX Homo sapiens.
XX
XX Saccharomyces cerevisiae.
XX
XX Synthetic.
XX
XX Chimeric.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..1440
XX /*tag= a
XX
XX sig_peptide
XX 1..15
XX /*tag= b
XX /note= "alpha-mating factor secretion signal"
XX
XX mat_peptide
XX 16..1437
XX /*tag= c
XX /product= "DR2-Fos-Fc"
XX
XX
XX WO9942597-A1.
XX
XX
XX 26-AUG-1999.
XX
XX 19-FEB-1999; 99WO-US003603.
XX
XX 19-FEB-1998; 98US-0075351P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Wuchterpfennig KW, Strominger JL;
XX
XX WPI; 1999-527481/44.
XX
XX P-PSDB; AAY31654.
XX
XX
XX New HMC Class II binding domain fusion proteins and conjugates - used
XX for, e.g. treating allergic and autoimmune diseases or detecting,
XX isolating, activating or killing specific T cells.
XX
XX Example 7; Page 100-102; 113pp; English.
XX
XX
XX This nucleotide sequence codes for a divalent HLA-DR2 MHC binding domain
XX fusion protein (see AAY31654) comprising an alpha-mating factor secretion
XX signal, the extracellular domain of the HLA-DR2 alpha chain (residues 1-
XX 191 of DRA*0101), a 7-amino acid linker, the 40-amino acid leucine zipper
XX dimerization domain of Fos, and the Fc portion of IgG2a. The DR-alpha-Fc
XX chain corresponds to an antibody heavy chain. The invention provides new
XX monovalent, multivalent and multimeric MHC Class II binding domain fusion
XX proteins and conjugates comprising at least a binding domain of an MHC
XX Class II alpha or beta chain and a dimerization domain, especially a Fos
XX or Jun leucine zipper domain. The MHC fusion proteins and conjugates can

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CC be used: for detecting and isolating T cells having a defined MHC/peptide
CC complex specificity (claimed); to confer to a subject adoptive immunity
CC to a defined MHC/peptide complex (claimed); to stimulate or activate T
CC cells reactive to a defined MHC/peptide complex (claimed); for selective
CC killing of T cells reactive to a defined MHC complex (claimed); to
CC tolerate a subject to a defined MHC/peptide complex (claimed); to treat
CC allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid
CC arthritis, pemphigus vulgaris, and systemic lupus erythematosus; and to
CC prevent organ or tissue transplant rejection. The DR2-IgG design was
CC chosen to increase the affinity for the T cell receptor by increasing
CC valency, and to attach an effector domain, the Fc region of IgG2a.
CC Complement fixation may result in the lysis of target T cells following
CC binding of DR2-IgG molecules to the T cell receptor. DR2-IgG molecules
CC may therefore be useful for the selective depletion of autoaggressive T
CC cells
XX
XX
XX Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

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Query Match 64.5%; Score 956.6; DB 2; Length 1446;
Best Local Similarity 81.8%; Pred. No. 1.8e-247;
Matches 1135; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

Qy 116 TTTATCAGTCTCTGGAGACATTTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGT 175
Db 50 TCTATCTGAATCTCTGACCAATCAGGCGAGTTTATGTTTGACTTTTGATGGTGATGAGATT 109
Qy 176 TCTATGTGGACTTTGGATAAGAAAGAAACTGCTGTGGAGGCTTCCTGAGTCTTGGCCAAATTGA 235
Db 110 TCCATGTGGATATGGCCAAAGAGAGACGGTCTGGCGGCTTGAAGAAATTTGGACGATTTG 169
Qy 236 TACTCTTTGAGCCCCCAAGTGGACTGCAAAACATAGCTGCAGAGAAAAACACAACCTTGGAA 295
Db 170 CCAGCTTTTGAGGCTCAAGGTGCATTGGCCAAACATAGCTGTGGACAAAGCCAACTTGGAAA 229
Qy 296 TCTTGACTAAGAGGTCAAATTTCAACCCAGCTACCAATGAGGCTCTCAAGCGAGCTGTGT 355
Db 230 TCATGACAAAGCGCTCCAACTATATCTCCGATCAACCAATGACCTCCAGAGGTAATCTGTGC 289
Qy 356 TCCCCAAGTCCCTGTGCTGCTGGTCAGCCCAACACCCCTTATCTGCTTTGTGACAAACA 415
Db 290 TCAGGAACAGCCCTGTGGAACTGAGAGAGCCCAACGCTCTCACTGTTTCATAGACAAGT 349
Qy 416 TCTTCCACCTGTGATCAACATCACAATGGCTGCAGAAATAGCAAGTCACTCAGACGCGCG 475
Db 350 TCACCCACCAGTGGTCAATGTCAAGTGTGCTCGAATGGAACACCTGTCAACACAGAG 409
Qy 476 TTTATGAGACAGCTTCTCTGTCACCGTGACCAATTCCTTCCACAACTGCTCTTATCTCA 535
Db 410 TGTCAAGACAGTCTTCTCTGCCAGGGAAGACCACTTTTCCGCAAGTTCACACTATCTCC 469
Qy 536 CTTTCATCCCTCTGTGATGATGACATTTATGACTGCAAGTGGAGCACTGGGGCTGGAGG 595
Db 470 CCTTCTCTGCCCTCAACTGAGAGCGTTTACGACTGCAGGTGGAGCACTGGGGCTTGGATG 529
Qy 596 AGCGGGTTCTGAAACACTGGGAACCTGAGATTCAGGCCCTCCCTGTCAGAGGTGACAGAAA 655
Db 530 AGCCTCTTCTCAAGCACTGGAGTTTGATGCTCCAAGCCCTCTCCCAAGAGACTACAGAGG 589
Qy 656 CTGGAGGTGAGGATCCACT-----ACAGCTCCATCAGCTCAGCTCGAATA 700
Db 590 TCGACGAGGTGGCGCGGTTTAACTGATACACTCCAAAGCGGAGACAGATCAACTTGAAG 649
Qy 701 AAGAGCTCCAGGCGCTGGGAAGGAATAATCAGAGCTGGAATGGGAGTTCAGAGCTGG 760
Db 650 ACAGAGAGTCTGCGTTGACAGACGAGATTCGCAATCTACTGAAAGAGAGAAAGAACTGG 709
Qy 761 AAAAGGAACCTG---GTCAGCGAGCACTCTGAGGCCAGAGGGGCCCAACATCAAGCCCTGTC 817
Db 710 AGTTTCATCTCGCGCGCCCATGCGAGCATCTGAGCCAGAGGGGCCCAACATCAAGCCCTGTC 769
Qy 818 CTCATGCAAAATGCCAGACACCTAAACCTCTTTGGGTGACCATCGGTCTTCATCTTCCTC 877
Db 770 CTCATGCAAAATGCCAGACACCTAAACCTCTTTGGGTGAGACCATCGGTCTTCATCTTCCTC 829

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QY 878 CAAAGATCAAGGATGTAATCATGATCTCCCTGAGCCCATAGTACATGTTGTGGTGG 937
Db 830 CAAAGATCAAGGATGTAATCATGATCTCCCTGAGCCCATAGTACATGTTGTGGTGG 889
QY 938 ATGTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTGTGTAACAACAGTGGAGTAC 997
Db 890 ATGTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTGTGTAACAACAGTGGAGTAC 949
QY 998 ACACAGCTCAGACACAAACCCATAGAGGATTACACAGTACTCTCCGGGTGGTCACTG 1057
Db 950 ACACAGCTCAGACACAAACCCATAGAGGATTACACAGTACTCTCCGGGTGGTCACTG 1009
QY 1058 CCTCCCATCCAGCACCAGGACTGATGAGTGGCAAGGTTCAATGCAAGGTCAACA 1117
Db 1010 CCTCCCATCCAGCACCAGGACTGATGAGTGGCAAGGTTCAATGCAAGGTCAACA 1069
QY 1118 ACAAAGACTCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1177
Db 1070 ACAAAGACTCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAG 1129
QY 1178 TTCCACAGGTATATGCTTGTGCTCCACAGAGAGAGATGACTAAGAAAACAGGTCACTC 1237
Db 1130 TTCCACAGGTATATGCTTGTGCTCCACAGAGAGAGATGACTAAGAAAACAGGTCACTC 1189
QY 1238 TGACCTGATGTCAGACTTCATGCTGAGGATTAAGACATTTACGTGAGTGGACCAACAG 1297
Db 1190 TGACCTGATGTCAGACTTCATGCTGAGGATTAAGACATTTACGTGAGTGGACCAACAG 1249
QY 1298 GGAAACACAGAGCTAAACTACAGAACACTGTAACACAGTCTGAGACTCTGATGTTCTTACT 1357
Db 1250 GGAAACACAGAGCTAAACTACAGAACACTGTAACACAGTCTGAGACTCTGATGTTCTTACT 1309
QY 1358 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAAGAAATAGTACTCCT 1417
Db 1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAAGAAATAGTACTCCT 1369
QY 1418 GTTCAGTGGTCCACAGGGTCTGCAATCACCACAGCACTAAGAGCTTCTCCCGGACTC 1477
Db 1370 GTTCAGTGGTCCACAGGGTCTGCAATCACCACAGCACTAAGAGCTTCTCCCGGACTC 1429
QY 1478 CGGGTAA 1484
Db 1430 CGGGTAA 1436
RESULT 5
ABI99027
ID ABI99027 standard; cDNA; 2346 BP.
XX
AC ABI99027;
XX
DT 25-FEB-2002 (first entry)
XX
DE IAS MBP 1-14 CH1.CH2.CH3 coding sequence.
XX
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200170245-A1.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-US009616.
XX
PR 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX
PA (CORI-) CORIXA CORP.
XX
Carter D, Zhu S, Arimilli S, Wang A;
PI
WPI; 2001-616371/71.
DR P-PSDB; ABB56457.
XX
Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha and beta domain linked through amino acid linker and multimerization domain.
PS Disclosure; Page 91-92; 147pp; English.
XX
The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha domain and a beta domain linked through an amino acid linker and a multimerization domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention
SQ Sequence 2346 BP; 560 A; 663 C; 646 G; 477 T; 0 U; 0 Other;
Query Match 48.9%; Score 725.2; DB 4; Length 2346;
Best Local Similarity 70.5%; Pred. No. 6.3e-185;
Matches 1094; Conservative 0; Mismatches 323; Indels 135; Gaps 4;
QY 68 GTGAAGACGACATGAGGCCGACACAGTAGGCTTCTATGTTACAACTGTTTATCAGTCTC 127
Db 779 GTGAAGACGACATGAGGCCGACACAGTAGGCTTCTATGTTACAACTGTTTATCAGTCTC 838
QY 128 CTGAGACATTTGGCCAGTACACATGAATTTGATGTTGATGAGTTGTTCTATGTTGACT 187
Db 839 CTGAGACATTTGGCCAGTACACATGAATTTGATGTTGATGAGTTGTTCTATGTTGACT 898
QY 188 TGGATAGAGAAACATGTTCTGGAGGCTTCTGAGTTTGGCCAATTGATCTCTTTGAGC 247
Db 899 TGGATAGAGAGGAGACTATCTGATGCTTCTGAGTTTGGCCAATTGATCTCTTTGAGC 958
QY 248 CCCAAGTGGAGTGCACAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGA 307
Db 959 CCCAAGTGGAGTGCACAAACATAGCTGCAGAAAAACATAGCTTGGAATCTTGACTAAGA 1018
QY 308 GGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCACTGTGTTCCCAAGTCCC 367
Db 1019 GGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCACTGTGTTCCCAAGTCCC 1078
QY 368 CTGTGCTGCTGGTCCAGCCCAACCCCTTATCTGCTTTGTGGACAACTCTTCCCACTG 427
Db 1079 CTGTGCTGCTGGTCCAGCCCAACCCCTTATCTGCTTTGTGGACAACTCTTCCCACTG 1138
QY 428 TGATCAACATCACATGGCTCAGAAATAGCAAGTCAAGTGCAGACAGCGGCTTTATGAGACA 487
Db 1139 TGATCAACATCACATGGCTCAGAAATAGCAAGTCAAGTGCAGACAGCGGCTTTATGAGACA 1198
QY 488 GCTTCTCTCGTCAACCGTGACCAATTCCTTTCCACAAAGTGTCTTTATCTACCTTCATCCCTT 547
Db 1199 GCTTCTCTCGTCAACCGTGACCAATTCCTTTCCACAAAGTGTCTTTATCTACCTTCATCCCTT 1258
QY 548 CTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGGTTCTGA 607
Db 1259 CTGATGATGATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGGTTCTGA 1318
QY 608 AACACTGGG-----AA 618
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Db 1319 AACACTGGGTAGCGGAGGGGCGGAAGCGCGGAGGGGAGCCAAACGACACCCCCCAT 1378
Qy 619 CCTGAGATTCAGGCCCCCATGTCTAGAGCTGACAGAA----- 654
Db 1379 CTGTCTATCCACTGGCCCTGGATCTGTGCTCCCAACTAACTCCATGGTGACCTGGAT 1438
Qy 655 -ACTGGAGTGGAGATCCACTACAGTCCATCAGTCTAGCTCGAAAGAGCTCCAGGC 713
Db 1439 GCCTGGTCAAGGGGTATTTCCCTGAGCCAGTGACAGTGCACCTGGAATCTGGATCCCTGT 1498
Qy 714 CCTGGAGAGGAAAT-----GCAAG 735
Db 1499 CCAGCGTGTGCACACCTTCCAGCTGTCTGAGTCTGACCTTACACTGTGAGCAGCT 1558
Qy 736 CTGGAATGGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCAGCATCTGAGCCGAGA 795
Db 1559 CAGTGACTGTCCCTCCAGCACCTGGCCGAGAGACCGTCACTGCAACGTTGCCACC 1618
Qy 796 GGGCCCAATCAAGCCCTGTCTCTCATGCAATGCCCAG----- 835
Db 1619 CGGCCAGCAGCACCAAGGTGGACAAGAAATTTGTGCCCAGGGATTGTGTTGAAGCCTT 1678
Qy 836 ---CACCTAACTCTTGGGTGGACCATCCGCTTTCATCTTCCCTCCAAAGATCAAGGATG 892
Db 1679 GCATATGTACAGTCCCAAGATATCATCTGTCTTTCATCTTCCCTCCAAAGCCCAAGGATG 1738
Qy 893 TACTCATGATCTCCCTGAGCCCATAGTCAATGTGTGGTGGATGTGAGCGAGGATG 952
Db 1739 TGCTCACCATTACTCTGACTCTTAAGGTCAAGTGTGTGTGGTAGACATCAGCAGGATG 1798
Qy 953 ACCAGATGTCAGATCAGCTGGTGTGTAACAACGTGGAGTACACAGCTCAGACAC 1012
Db 1799 ATCCGAGGTCCAGTTCAGCTGGTGTGTAGATGATGTGGAGTGCACACAGCTCAGACGC 1858
Qy 1013 ARAACCATAGAGAGATTACAACAGTACTCTCCGGGTGGTCAAGTCCCTCCCATCCAGC 1072
Db 1859 AATCCCGGAGGAGCAGTCAACAGCACCTTTCGCTCAGTCAGTGAACCTTCCCATATGC 1918
Qy 1073 ACCAGGACTGGATGAGTGGCAAGGATTCAATCAAGGTCAACACAAAGACTCCCCAG 1132
Db 1919 ACCAGGACTGGCTCAATGGCAAGGATTCAATGCAGGTTCAACAGTGCAGCTTTCCTG 1978
Qy 1133 CGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGAGTCCACAGATATATG 1192
Db 1979 CCCCCATCGAAGAAACCATCTCCAAACCCAAAGGTCAGTAAGGCTCCACAGGTGACA 2038
Qy 1193 TCTGTCTCCACAGAGAGAGATGACTAAGAACAGGTCACTCTGACCTGCATGTGCA 1252
Db 2039 CCATTCACCTCCCAAGGAGCAGATGGCCCAAGGATNAAGTCAGTCTGACCTGCATGATA 2098
Qy 1253 CAGACTTCATGCTCGAAGACATTTACGTGGAGTGGACCAACAAAGGAAACAGAGCTAA 1312
Db 2099 CAGACTTCTTCCCTGAAGACATTTACTGTGAGTGGCAGTGGATGGCAGCAGCGAGA 2158
Qy 1313 ACTACAAGAACACTGAACCAAGTCTCGACTCTGATGTTCTTACTTCATGTGTACAGCAAGC 1372
Db 2159 ACTACAAGAACACTCAGCCCATCATGTGACACAGATGCTCTTACTTCTGTACAGCAAGC 2218
Qy 1373 TGAGAGTGGAAAGAGAACTGGGTGGAGAAAGAAATGACTACTCTCTGTTCAGTGTGTCAGC 1432
Db 2219 TCAATGTGCAAGAGAGCAACTGGGAGGACAGAAATATCTTTTCACTGCTCTGTGTACATG 2278
Qy 1433 AGGCTCTGCAAAATFACACACAGACTTAAGAGCTTCTCCCGAGCTCCGGGTAA 1484
Db 2279 AGGCTCTGCAAAACCAACCATCTAGAGAGAGGCTCTTCCCACTCTCTCTGGTAA 2330
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RESULT 6

ABI99033

ID ABI99033 standard; cDNA; 2343 BP.

XX

AC ABI99033;

XX

25-FEB-2002 (first entry)

MBP 90-101 CH1.H.CH2.CH3 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
single chain; immunosuppressive; antidiabetic; antiinflammatory;
antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
autoimmune disease; insulin dependent diabetes; multiple sclerosis;
myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.

Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.

15-MAY-2000; 2000US-0204249P.

23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.

P-PSDB; ABB56463.

Multimeric complex for treating autoimmune diseases, comprises first and
second single chain MHC class II molecules, each comprising alpha and
beta domain linked through amino acid linker and multimerization domain.
Disclosure; Page 96; 147pp; English.

The invention relates to a multimeric complex comprising a first
recombinant single chain major histocompatibility complex (MHC) class II
molecule and a second recombinant single chain MHC class II molecule,
each comprising an alpha domain and a beta domain linked through an
amino acid linker and a multimerization domain. The first and the second
molecule are linked through the multimerization domain to form a
multimeric complex. The complex is useful for treating autoimmune
diseases. It is useful for treating insulin dependent diabetes, multiple
sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
erythematosus. The present sequence encodes a single chain MHC class II
molecule of the invention

SQ Sequence 2343 BP; 562 A; 665 C; 635 G; 481 T; 0 U; 0 Other;

Query Match 48.7%; Score 722.2; DB 4; Length 2343;

Best Local Similarity 70.4%; Pred. No. 4.1e-184;

Matches 1094; Conservative 0; Mismatches 323; Indels 138; Gaps 4;

Qy 68 GTGAAGACGACATTGAGGCGGACACGCTAGGCTTCTATGTACAACTGTTTATCAGTCTC 127

Db 773 GTGAAGACGACATTGAGGCGGACACGCTAGGCTTCTATGTACAACTGTTTATCAGTCTC 832

Qy 128 CTGGAGACATTTGGCCAGTACACATGAAATTTGATGGTATGATGTTCTTATGTGAGCT 187

Db 833 CTGGAGACATTTGGCCAGTACACATGAAATTTGATGGTATGATGTTCTTATGTGAGCT 892

Qy 188 TGATTAAGAGAAACCTGCTGGAGGCTTCTGAGTTGGCCAAATTAATCTTTTGGAGC 247

Db 893 TGGTAAGAGAGGAGACTATCTGGATGCTTCTGAGTTTGGCCAAATTCACAGCTTTGACC 952

Qy 248 CCCAAGGTGAGCTGCAAAACATAGCTGCAGAAAACAACTTGGGAATCTTGACTAAGA 307

Db 953 CCCAAGGTGAGCTGCAAAACATAGCTGCAGAAAACAACTTGGGAATCTTGACTAAGA 1012

Qy 308 GGTCAAAATTTTCCAGCCAGCTTACCAATGAGGCTCTCTCAAGCGAGCTGTGTTCCCCAAGTCCC 367

QY 1060 CTCCCATCCAGCACCAGGACTGGATGATGGCCAGAGGATTCAATGCAAGGTCAACAA 1119
Db 679 CTCCCATCCAGCACCAGGACTGGATGATGGCCAGAGGATTCAATGCAAGGTCAACAA 738
QY 1120 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 1179
Db 739 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 798
QY 1180 CCACAGGTATATGTCTTCCCTCCACGAGAGAGATGACTTAAGAAACAGGTCACTCTG 1239
Db 799 CCACAGGTATATGTCTTCCCTCCACGAGAGAGATGACTTAAGAAACAGGTCACTCTG 858
QY 1240 ACCTGCATGGTCACAGACTTCATGCTGAGACATTTACGTGGAGTGACCAACACGGG 1299
Db 859 ACCTGCATGGTCACAGACTTCATGCTGAGACATTTACGTGGAGTGACCAACACGGG 918
QY 1300 AAAACAGAGCTAAATCTACAAGAACTGAACCACTGCAACAGTCTGATGGTCTTACTTC 1359
Db 919 AAAACAGAGCTAAATCTACAAGAACTGAACCACTGCAACAGTCTGATGGTCTTACTTC 978
QY 1360 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGT 1419
Db 979 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGT 1038
QY 1420 TCAGTGGTCCACGAGGGTCTGCAGAACTCACACACAGCTTAAGAGCTTCTCCGGACTCCG 1479
Db 1039 TCAGTGGTCCACGAGGGTCTGCAGAACTCACACACAGCTTAAGAGCTTCTCCGGACTCCG 1098
QY 1480 GGTA 1484
Db 1099 GGTA 1103

RESULT 9
ADO07577
ID ADO07577 standard; DNA; 1108 BP.
XX ADO07577;
AC ADO07577;
DT 15-JUL-2004 (first entry)
XX Fusion protein coding sequence fragment Igk8.
DE immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW neuroprotective; antipsoriatic; dermatological; antiinflammatory;
KW cytostatic; interleukin-15; immunoglobulin G; ds; gene.
XX Synthetic.
OS Unidentified.
XX WO2004035622-A2.
PN 29-APR-2004.
PD 13-OCT-2003; 2003WO-CH0000666.
XX 14-OCT-2002; 2002EP-00022869.
PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA Dreher I, Moll T;
XX WPI; 2004-357203/33.
DR New fusion protein of interleukin-15 and Fc fragment, useful for treating
PT e.g. transplantation disorders, autoimmune diseases and tumors, also
PT related nucleic acid.
XX Disclosure; Fig 10; 63pp; German.
PS The present invention relates to a fusion protein consisting of wild-type
CC interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other

CC than a murine IgG2b Fc fragment. The fusion proteins and coding sequences
CC are used to prevent or treat consequences of transplantation and/or
CC autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple
CC sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumors and
CC AIDS, etc., and tissues or organs that express the protein are useful for
CC transplantation into humans or other mammals, as allo-, auto- or xeno-
CC transplants. Also transgenic animals that express the fusion proteins are
CC useful as source of cells, tissues and organs for transplantation or to
CC screen for pharmaceuticals and/or to identify toxic substances. The
CC present sequence is a coding sequence used in the exemplification of the
CC invention.

SQ Sequence 1108 BP; 342 A; 255 C; 254 G; 257 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.2; DB 12; Length 1108;
Best Local Similarity 93.2%; Pred. No. 2.6e-178;
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 700 AAAGAGCTCCAGCGCCCTGGAGAGGAAATGCACAGCTGGAATGGAGTTGCAAGCACTG 759
Db 319 AAAGAGCTGGAGAACTGGAGGAAATATTAAGAAATTTTGGACAGTTTGTATCAT 378
QY 760 GAAAGAGAACTGGCTCAGGCAGCATCTGAGCCCGAGAGGGCCCAATCAAGCCCTGTCT 819
Db 379 ATTGTCGACATGTTTCATCAACACTTCGGATCCGAGAGGGCCCAATCAAGCCCTGTCT 438
QY 820 CCATGCAAAATGCCAGACACTTAACCTCTTGGGTGGACCATCCGTCTTCATCTCCCTCA 879
Db 439 CCATGCAAAATGCCAGACACTTAACCTCTTGGGTGGACCATCCGTCTTCATCTCCCTCA 498
QY 880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGTGTGTGAT 939
Db 499 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGTGTGTGAT 558
QY 940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTGTGTGTGTGTGTGTGTGTGTGT 999
Db 559 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTGTGTGTGTGTGTGTGTGTGTGT 618
QY 1000 ACAGCTCAGACACAAACCCATAGAGAGATTACAAAGTACTCTCCGGGTGGTCAAGTCC 1059
Db 619 ACAGCTCAGACACAAACCCATAGAGAGATTACAAAGTACTCTCCGGGTGGTCAAGTCC 678
QY 1060 CTCCCATCCAGCACCAGGACTGGATGATGGCCAGAGGATTCAATGCAAGGTCAACAA 1119
Db 679 CTCCCATCCAGCACCAGGACTGGATGATGGCCAGAGGATTCAATGCAAGGTCAACAA 738
QY 1120 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 1179
Db 739 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 798
QY 1180 CCACAGGTATATGTCTTCCCTCCACGAGAGAGATGACTTAAGAAACAGGTCACTCTG 1239
Db 799 CCACAGGTATATGTCTTCCCTCCACGAGAGAGATGACTTAAGAAACAGGTCACTCTG 858
QY 1240 ACCTGCATGGTCACAGACTTCATGCTGAGACATTTACGTGGAGTGACCAACACGGG 1299
Db 859 ACCTGCATGGTCACAGACTTCATGCTGAGACATTTACGTGGAGTGACCAACACGGG 918
QY 1300 AAAACAGAGCTAAATCTACAAGAACTGAACCACTGCAACAGTCTGATGGTCTTACTTC 1359
Db 919 AAAACAGAGCTAAATCTACAAGAACTGAACCACTGCAACAGTCTGATGGTCTTACTTC 978
QY 1360 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGT 1419
Db 979 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGT 1038
QY 1420 TCAGTGGTCCACGAGGGTCTGCAGAACTCACACACAGCTTAAGAGCTTCTCCGGACTCCG 1479
Db 1039 TCAGTGGTCCACGAGGGTCTGCAGAACTCACACACAGCTTAAGAGCTTCTCCGGACTCCG 1098
QY 1480 GGTA 1484
Db 1099 GGTA 1103

RESULT 10	
ADL15694	
ID	ADL15694 standard; DNA; 990 BP.
XX	
AC	ADL15694;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Murine immunoglobulin heavy chain constant region DNA SeqID 68.
XX	
DE	mouse; murine; antibody; gene; ds; beta-amyloid; A-beta;
KW	amyloid beta A4 precursor protein; APP; presenilin;
KW	lipoprotein receptor related protein; LRP; beta-amyloid 42; A-beta 42;
KW	Alzheimer's disease; neuroprotective; nootropic.
XX	
OS	Mus musculus.
XX	
PN	WO2004018997-A2.
XX	
XX	04-MAR-2004.
XX	
PF	20-AUG-2003; 2003WO-US026173.
XX	
PR	20-AUG-2002; 2002US-0405417P.
PR	18-SEP-2002; 2002US-0411974P.
XX	
PA	(NEUR-) NEUROGENETICS INC.
XX	
PI	Kounnas M, Patrick A, Velicelebi G, Wagner S;
XX	
DR	WPI; 2004-226902/21.
DR	P-PSDB; ADL15695.
XX	
PT	New polypeptide comprises a sequence of amino acids that is selectively
PT	reactive with beta-amyloid peptide 42 or at least one complementarity-
PT	determining region of antibody A387 or B436, useful for treating
PT	Alzheimer's disease.
XX	
PS	Disclosure; SEQ ID NO 68; 408pp; English.
XX	
CC	This invention relates to novel methods and compositions for detecting
CC	and modulating beta-amyloid (A-beta) peptide levels and the processing of
CC	amyloid beta A4 precursor protein (APP). Specifically, it refers to
CC	methods of assessing the presenilin activity of compounds using the
CC	lipoprotein receptor related protein (LRP), in order to identify
CC	presenilin proteins that can be used to affect the processing of APP. The
CC	present invention describes methods to identify agents that modulate
CC	presenilin activity and A-beta levels, in particular beta-amyloid 42 (A-
CC	beta 42), such that the agent is selectively reactive with A-beta 42 and
CC	binds at least one complementarity determining region (CDR) of either
CC	antibody A387 or antibody B436. As such, the polypeptides, nucleic acids
CC	and antibodies are useful for treating Alzheimer's disease, accordingly
CC	the compositions exhibit neuroprotective and nootropic activities. This
CC	polynucleotide sequence is a murine antibody chain DNA fragment of the
CC	invention.
XX	
SQ	Sequence 990 BP; 274 A; 286 C; 235 G; 195 T; 0 U; 0 Other;
Query Match	47.1%; Score 699.6; DB 12; Length 990;
Best Local Similarity	100.0%; Pred. No. 3.6e-178;
Matches 699; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	786 TGAGCCAGAGGGCCCAATCAAGCCCTGCTCCATGCAAAATGCCAGACCTAACCT 845
DB	291 TGAGCCAGAGGGCCCAATCAAGCCCTGCTCCATGCAAAATGCCAGACCTAACCT 350
QY	846 CTTGGGTGGACCACTCGCTCTTCTCTCCATGCAAAATGCCAGACCTAACCT 905
DB	351 CTTGGGTGGACCACTCGCTCTTCTCTCCATGCAAAATGCCAGACCTAACCT 410
QY	906 CCTGAGCCCCATAGTCACATGTGTGGTGGATGTGAGCGGAGGTGACCCAGATGTCCA 965

Db	411	CCTGAGCCCCATAGTCACATGTGTGGTGGATGTGAGCGGAGGTGACCCAGATGTCCA	470
QY	966	GATCAGCTGTTTGTGAACACGTGGAGTACACACAGCTCAGACACAAACCCATAGAGA	1025
DB	471	GATCAGCTGTTTGTGAACACGTGGAGTACACACAGCTCAGACACAAACCCATAGAGA	530
QY	1026	GGATTACACACAGTACTCTCCGGGTGGTTCAGTGGCCCTCCCATCCAGACACAGGACTGGAT	1085
DB	531	GGATTACACACAGTACTCTCCGGGTGGTTCAGTGGCCCTCCCATCCAGACACAGGACTGGAT	590
QY	1086	GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGCGGCCCATCGAGAG	1145
DB	591	GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGCGGCCCATCGAGAG	650
QY	1146	AACCATCTCAAAACCCCAAGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCCTCCACC	1205
DB	651	AACCATCTCAAAACCCCAAGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCCTCCACC	710
QY	1206	AGAAGAGAGATGACTAAGAAACAGAGTCACTCTGACCTGCATGGTTCACAGACTTTCATGCC	1265
DB	711	AGAAGAGAGATGACTAAGAAACAGAGTCACTCTGACCTGCATGGTTCACAGACTTTCATGCC	770
QY	1266	TGAAGACATTTACGTGGAGTGGACCAACACCGGAAACACAGAGCTAACTACAAAGAACAC	1325
DB	771	TGAAGACATTTACGTGGAGTGGACCAACACCGGAAACACAGAGCTAACTACAAAGAACAC	830
QY	1326	TGAACCACTCTGGACTCTCATGGTCTTCTTACTTATCATGTACAGCAAGCTGAGAGTGGAAA	1385
DB	831	TGAACCACTCTGGACTCTCATGGTCTTCTTACTTATCATGTACAGCAAGCTGAGAGTGGAAA	890
QY	1386	GAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTCAAGTGGTCCACGAGGTCTGCACAA	1445
DB	891	GAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTCAAGTGGTCCACGAGGTCTGCACAA	950
QY	1446	TCACCAACAGCACTAAGAGCTTCTCCCGAGCTCCCGGGTAA	1484
DB	951	TCACCAACAGCACTAAGAGCTTCTCCCGAGCTCCCGGGTAA	989

RESULT 11	
AAQ12637	
ID	AAQ12637 standard; DNA; 1570 BP.
XX	
AC	AAQ12637;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-1991 (first entry)
XX	
DE	Monoclonal antibody OK3T heavy chain coding sequence.
XX	
KW	OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.
OS	Mus musculus.
XX	
Key	Location/Qualifiers
FT	sig_peptide 41..97
FT	/*tag= a
FT	mat_peptide 98..1447
FT	/*tag= b
FT	/product= "OK3T heavy chain"
XX	
PN	WO9109967-A.
XX	
PD	11-JUL-1991.
XX	
PF	21-DEC-1989; 89GB-00028874.
XX	
PR	21-DEC-1989; 89GB-00028874.
XX	
PR	21-DEC-1990; 90WO-GH002017.
XX	
PA	(CLLT) CELLTech LTD.
XX	

Db 661 CACATACACACACGACTAAGAGCTTCTCCCGGACTCCGGGTAA 704
|||||

RESULT 14

AD85817
ID ADE85817 standard; cDNA; 1140 BP.

XX AC ADE85817;
XX DT 29-JAN-2004 (first entry)

XX DE Murine interleukin-21/Fc fusion gene.
XX KW Mouse; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
XX KW antinflammatory; dermatological; ophthalmological; uropathic;
XX KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;
XX KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy;
XX KW antibody; antibody; gene; ss.

XX OS Chimeric.
XX MS Mus sp.

XX FH Key Location/Qualifiers
XX FT 1. 1140
XX FT /tag= a
XX FT /product= "IL-21/Fc fusion"

XX PN WO2003087320-A2.

XX PD 23-OCT-2003.

XX PF 08-APR-2003; 2003WO-US010736.

XX PR 09-APR-2002; 2002US-0371038P.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Moll T, Strom TB, Zheng XX;

XX WPI; 2003-845317/78.

XX DR P-PSDB; ADE85818.

XX CC New substantially pure interleukin-21 polypeptide, useful for diagnosing,
XX PT treating and prognosticating autoimmune disorders, e.g. rheumatic
XX PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
XX PT and myasthenia gravis.

XX PS Disclosure; SEQ ID NO 10; 65pp; English.

XX CC The present sequence is the coding sequence for a fusion protein
XX CC comprising murine interleukin-21 (IL-21) and an immunoglobulin Fc
XX CC polypeptide. Murine IL-21/Fc is capable of transducing signals through
XX CC the murine IL-21 receptor, has an increased in vivo serum half-life and
XX CC can activate complement mediated lysis or antibody-dependent cellular
XX CC cytotoxicity. The invention provides antagonists of the IL-21 receptor.
XX CC These include mutants of murine IL-21 and additionally comprise a
XX CC sequence that increases circulating half-life, such as the Fc region of
XX CC an IgG molecule. Such antagonists inhibit cellular proliferation in
XX CC response to either anti-CD3 monoclonal antibodies or anti-CD3 antibodies
XX CC applied together with IL-2 and/or IL-15 together with IL-21. A claimed
XX CC method of suppressing the immune response in a patient comprises
XX CC administering the IL-21 antagonist or a nucleic acid encoding it. The
XX CC method is used to treat an autoimmune disease such as rheumatic disease,
XX CC including systemic lupus erythematosus, Sjogren's syndrome, scleroderma,
XX CC mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's
XX CC syndrome, or Behcet's disease, or rheumatoid arthritis, type I diabetes,
XX CC autoimmune disease of the thyroid such as Hashimoto's thyroiditis or
XX CC Graves' disease, an autoimmune disease of the central nervous system such
XX CC as multiple sclerosis, myasthenia gravis, or encephalomyelitis, or an
XX CC autoimmune disease selected from pemphigus vulgaris, pemphigus vegetans,
XX CC pemphigus foliaceus, Senechal-Usher syndrome, Brazilian pemphigus,
XX CC psoriasis or inflammatory bowel disease (all claimed).

XX SQ Sequence 1140 BP; 344 A; 296 C; 264 G; 236 T; 0 U; 0 Other;
Query Match 47.1%; Score 699.2; DB 10; Length 1140;
Best Local Similarity 97.5%; Pred. No. 4.9e-178;
Matches 710; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 757 CTGGAAAGGAACCTGGCTCAGGCGAGCATCTCAGCCCGAGGGCCACAAATCAAGCCCTGT 816
DB 409 CTTCAAAAGATGATTCATCAGCATCTCTCAGATCCAGAGGGCCACAAATCAAGCCCTGT 468
QY 817 CCTCATGCAAAATGCCAGACCACTTCTTTGGTGAGCACCATCCGTCTTCATCTTCCCT 876
DB 469 CTTCAATCAAAATGCCAGACCACTTCTTTGGTGAGCACCATCCGTCTTCATCTTCCCT 528
QY 877 CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGTGTGGTG 936
DB 529 CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGTGTGGTG 588
QY 937 GATGTGAGGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAAACAACGTGGAAGTA 996
DB 589 GATGTGAGGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAAACAACGTGGAAGTA 648
QY 997 CACACAGCTCAGACACAAACCCATAGAGAGATTACAAACAGTACTCTCCGGGTGTCTAGT 1056
DB 649 CACACAGCTCAGACACAAACCCATAGAGAGATTACAAACAGTACTCTCCGGGTGTCTAGT 708
QY 1057 GCCCTCCCATCCAGCACCCAGGACTGGATGATGGCAAGGAGTTCAAATGCAAGGTCAAC 1116
DB 709 GCCCTCCCATCCAGCACCCAGGACTGGATGATGGCAAGGAGTTCAAATGCAAGGTCAAC 768
QY 1117 AACAAAGACCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1176
DB 769 AACAAAGACCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
QY 1177 GCTCCACAGGTATATGTCTTGCTCCACAGAGAGAGATGACTTAAGAAACAGGTCACT 1236
DB 829 GCTCCACAGGTATATGTCTTGCTCCACAGAGAGAGATGACTTAAGAAACAGGTCACT 888
QY 1237 CTGACCTGCATGGTCAACAGACTTTCATGCTGAAAGACATTTACGTGGAGTGAGCAACAAAC 1296
DB 889 CTGACCTGCATGGTCAACAGACTTTCATGCTGAAAGACATTTACGTGGAGTGAGCAACAAAC 948
QY 1297 GGGAAACAGAGCTAAACTACAGACACTGAACCCAGTCTCTGGACTCTGTAGTGTCTTAC 1356
DB 949 GGGAAACAGAGCTAAACTACAGACACTGAACCCAGTCTCTGGACTCTGTAGTGTCTTAC 1008
QY 1357 TTCAATGTACAGCAAGCTGAGAGTGGAAAGAGAACTGGGTGGAAAGAAATAGCTACTCC 1416
DB 1009 TTCAATGTACAGCAAGCTGAGAGTGGAAAGAGAACTGGGTGGAAAGAAATAGCTACTCC 1068
QY 1417 TGTTTCAGTGGTCCAGAGGGGTCTGCACAATCACCACAGACTTAAGAGACTTCTCCCGGACT 1476
DB 1069 TGTTTCAGTGGTCCAGAGGGGTCTGCACAATCACCACAGACTTAAGAGACTTCTCCCGGACT 1128
QY 1477 CCGGGTAA 1484
DB 1129 CCGGGTAA 1136
RESULT 15
ID AAT59350 standard; DNA; 1158 BP.
XX AC AAT59350;
XX DT 07-MAY-1997 (first entry)
XX DE 1-153 delta 112-115 c-mpl ligand-mouse Fc fusion gene.
XX KW c-mpl ligand; Megakaryocyte Growth and Development Factor; MGDF;
XX KW thrombopoietin; TPO; variant; mutein; chimera; increased activity;
XX KW decreased side effect; ex vivo expansion; stem cell; treatment;

haematopoietic disorder; gene therapy; human; ss.

XX Synthetic.

OS Mus sp.

OS Chimeric.

XX WO9623888-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 96WO-US000830.

XX 03-FEB-1995; 95US-00383035.

XX (SEAR) SEARLE & CO G D.

XX Staten NR, Favara JP, Kahn LE, Baum CM, Pegg LE, McKearn JP;

XX WPI; 1996-371436/37.

XX P-PSDB; AAW01765.

XX Mutant c-mpl ligands - used for stimulating the prodn. of haematopoietic

XX cells and in the treatment of haematopoietic disorders.

XX Claim 20; Page; 74pp; English.

XX This DNA sequence, isolated from BHK expression plasmid pMON26465,

XX encodes amino acids 1-153 of c-mpl ligand with a deletion of residues 112

XX -115 fused to a mouse Fc fragment. The native c-mpl ligand is also

XX referred to as Megakaryocyte Growth and Development Factor (MGDF) or

XX thrombopoietin (TPO). Variants of c-mpl ligand can have an

XX improved biological profile, such as increased activity and/or decreased

XX side effects, and/or improved physical properties, such as improved half-

XX life, stability and/or re-fold efficiencies. They can be used for

XX selective ex vivo expansion of stem cells, for the treatment of patients

XX having a haematopoietic disorder or in human gene therapy

XX SQ Sequence 1158 BP; 299 A; 333 C; 291 G; 235 T; 0 U; 0 Other;

Query Match

Best Local Similarity 47.1%; Score 699; DB 2; Length 1158;

Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 TGAGCCAGAGGGCCACAAATCAAGCCCTGCTCCATGAAATGCCAGCACCTAACCT 845

DB 459 TGAGCCAGAGGGCCACAAATCAAGCCCTGCTCCATGAAATGCCAGCACCTAACCT 518

QY 846 CTTGGGTGGACCAATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGATCATGATCTC 905

DB 519 CTTGGGTGGACCAATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGATCATGATCTC 578

QY 906 CTTGAGCCCAATGATCATGCTGCTGGTGGATGTGAGGAGGATACCCAGATGTCCA 965

DB 579 CTTGAGCCCAATGATCATGCTGCTGGTGGATGTGAGGAGGATACCCAGATGTCCA 638

QY 966 GATCAGCTGTTGTGAACACGTTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025

DB 639 GATCAGCTGTTGTGAACACGTTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 698

QY 1026 GGATTACACAGTACTCTCCGGGTGGTCACTGCTCCCTCCATCCAGCACCCAGGACTGGAT 1085

DB 699 GGATTACACAGTACTCTCCGGGTGGTCACTGCTCCCTCCATCCAGCACCCAGGACTGGAT 758

QY 1086 GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGGCGCCATCGAGAG 1145

DB 759 GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGGCGCCATCGAGAG 818

QY 1146 AACCATCTCAAAACCCAAAGGTCAGTAAGGCTCCAGGTATATGCTTGTGCTCCACC 1205

DB 819 AACCATCTCAAAACCCAAAGGTCAGTAAGGCTCCAGGTATATGCTTGTGCTCCACC 878

QY 1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGATGGTCAAGACTTCATGCC 1265

Db 879 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGATGTCAAGACTTCATGCC 938

QY 1266 TGAAGACATTTTACCTGTGAGTGGACCAACAAACGGGAAACAGAGCTAAACTACAAGAACAC 1325

Db 939 TGAAGACATTTTACCTGTGAGTGGACCAACAAACGGGAAACAGAGCTAAACTACAAGAACAC 998

QY 1326 TGAACCAAGTCTCTGAGTCTCTGATGGTTCTTACTTCACTGATAGCAAGCTGAGAGTGGAAAA 1385

Db 999 TGAACCAAGTCTCTGAGTCTCTGATGGTTCTTACTTCACTGATAGCAAGCTGAGAGTGGAAAA 1058

QY 1386 GAAAGAACTGGGTGGAAAGAAATAGCTACTCTGTTCACTGGTCCACGAGGGTCTGCACAA 1445

Db 1059 GAAAGAACTGGGTGGAAAGAAATAGCTACTCTGTTCACTGGTCCACGAGGGTCTGCACAA 1118

QY 1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA 1484

Db 1119 TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA 1157

Search completed: June 19, 2005, 11:25:31

Job time : 889 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 16, 2005, 01:33:12 ; Search time 224.5 Seconds

(without alignments)
5113.162 Million cell updates/sec

Title: US-10-048-116-1

Perfect score: 2695

Sequence: 1 atgcgcgtgcagcagagctct.....ttctccgcgactccgggtaa 1484

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlp
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-DB=A_Geneseq -QMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45
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-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Desc04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2655	98.5	494	AAB67480	Aab67480 A fusion
2	2242	83.2	551	ABBS6471	Abbs6471 Murine pc
3	1919.5	71.2	479	AAY31654	Aay31654 HLA-DR2 a
4	1733	64.3	774	ABBS56431	Abbs56431 IAS MBP 1
5	1732.5	64.3	772	ABBS56463	Abbs56463 IAS MBP 9
6	1521	56.4	676	ABBS56458	Abbs56458 IAS MBP 1
7	1521	56.4	678	ABBS56457	Abbs56457 IAS MBP 1
8	1327	49.2	426	ADLI15170	Adli15170 Murine mo
9	1319.5	49.0	469	AAR40384	Aar40384 Monoclonal
10	1313.5	48.7	468	AAR13061	Aar13061 Monoclonal

11	1313.5	48.7	468	8	ADQ91057	Adq91057 Murine OK
12	1311.5	48.7	329	8	ADLI15695	Adli15695 Murine im
13	1310.5	48.6	477	2	AAR47450	Aar47450 T84.12 He
14	1306.5	48.5	329	8	ADLI15169	Adli15169 Murine im
15	1305.5	48.4	447	1	AAP93037	Aap93037 ChimERIC
16	1303.5	48.4	451	8	ADN97545	Adn97545 Artificia
17	1280.5	47.5	379	7	ADE85818	Ade85818 Murine in
18	1275	47.3	347	8	ADO07559	Ado07559 Fusion pr
19	1274.5	47.3	379	7	ADBS5820	Adebs5820 Murine mu
20	1272	47.2	357	2	AAW35863	Aaw35863 Human CTL
21	1270	47.1	347	8	ADO07563	Ado07563 Fusion pr
22	1270	47.1	347	8	ADO07564	Ado07564 Fusion pr
23	1270	47.1	367	8	AAW35862	Aaw35862 Human CD2
24	1270	47.1	486	5	AAEI13743	Aaei13743 Mouse Fal
25	1266.5	47.0	378	2	AAW35864	Aaw35864 Human FAS
26	1266	47.0	396	2	AAW01764	Aaw01764 1-153 c-m
27	1265.5	47.0	377	7	AAW78124	Aaw78124 ChimERIC
28	1265.5	47.0	377	7	ADFI1314	Adfi1314 Progenipo
29	1265	46.9	568	3	AAAY49935	Aay49935 Human gly
30	1264	46.9	322	7	ABR42615	Abr42615 Fusion pr
31	1264	46.9	425	2	AAW14763	Aaw14763 Mouse sol
32	1263.5	46.9	322	7	ABR42616	Abr42616 Fusion pr
33	1263	46.9	233	3	AAAY70359	Aay70259 Murine im
34	1263	46.9	233	3	AAAY49934	Aay49934 Human gly
35	1263	46.9	233	3	AAAY95580	Aay95580 Mouse imm
36	1263	46.9	233	7	ABR42614	Abr42614 Fusion pr
37	1263	46.9	386	2	AAW01765	Aaw01765 1-153 (de
38	1263	46.9	392	2	AAW01763	Aaw01763 1-153 del
39	1262.5	46.8	398	2	AAW78123	Aaw78123 ChimERIC
40	1262.5	46.8	398	7	ADFI1313	Adfi1313 Progenipo
41	1258.5	46.7	489	4	AAAB67719	Aab67719 Amino aci
42	1258	46.7	232	8	ADO07562	Ado07562 Fusion pr
43	1253.5	46.5	410	2	AAW35860	Aaw35860 Human CD4
44	1250.5	46.4	418	2	AAW35861	Aaw35861 Human CD2
45	1249	46.3	379	4	AAAB67716	Aab67716 Amino aci

ALIGNMENTS

RESULT 1

AAB67480
ID AAB67480 standard; protein; 494 AA.

XX

AC AAB67480;

DT 15-MAY-2001 (first entry)

XX

DE A fusion protein comprising an alpha chain of MHC.

XX

KW Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;

KW major histocompatibility complex; Fc region; antigen; T lymphocyte;

KW immunostimulant; vaccine; infection; tumour.

XX

OS Synthetic.

XX

PN WO200109194-A1.

XX

PD 08-FEB-2001.

XX

PF 28-JUL-2000; 2000WO-FR002193.

XX

PR 29-JUL-1999; 99PR-00009862.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Glaichenhaus N, Malherbe L;

XX

DR WPI; 2001-182944/18.

XX

DR N-PSDB; AAF55098.

XX

PT New soluble recombinant protein, useful e.g. as immunostimulant,

PT comprises dimeric major histocompatibility complex molecule fused to

PT immunoglobulin Fc region.

XX PS XX Example 1; Page 31-33; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence represents a recombinant protein of the invention, comprising an alpha chain of MHC molecules

SQ Sequence 494 AA;

Alignment Scores:

Pred. No.:	3,48e-215	Length:	494
Score:	2655.00	Matches:	494
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.52%	Indels:	0
DB:	4	Gaps:	0

US-10-048-116-1 (1-1484) x AAB67480 (1-494)

Qy 1 ATGCGGTGACAGAGCTGTGATCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTC 60

Db 1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu 20

Qy 61 TGGCGAGGTGAAGACGACATTGAGCGCCGACACCTAGGCTTCTATGGTACACCTGTTTAT 120

Db 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrValTyr 40

Qy 121 CAGTCTCTGAGACATTTGGCCAGCTACACATCAATTTGATGGTGTAGTCTTCTTAT 180

Db 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60

Qy 181 GTGACTTGGATAGAGAAACCTGTCTGGAGGCTTCTGAGGTTGGCCAAATGATCTC 240

Db 61 ValAspLeuAspLysLysThrValTyrArgLeuProGluPheGlyGlnLeuIleLeu 80

Qy 241 TTTGAGCCCCAAGTGGACTGCNAACATAGCTGCAGAAACACAACTTGGGAATCTTG 300

Db 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu 100

Qy 301 ACTAAGAGGTCAAATTTCAACCCAGCTACCAATCAGGCTCTCAAGCGACTGTGTTCCCC 360

Db 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120

Qy 361 AAGTCCCTGTGCTGTGGTGCAGCCCAACCTTATCTGCTTTGTGGACAAATCTTC 420

Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140

Qy 421 CCACCTGTGATCAACATCAGCTGCTCAGAAATAGCAAGTCAGTCACAGCGCGTTTAT 480

Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160

Qy 481 GAGACCACTCTCTCGTCAACCGTGACCATTTCCCTTCCACAAAGCTGTCTTCTCACCTTC 540

Db 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180

Qy 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGAGCGG 600

Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200

Qy 601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTGTCAGAGCTGCACAGAACTGGA 660

Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220

Qy 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGCGCCTGGAG 720

Db 221 GlyGlyGlySerThrAlaProSerAlaGlnLeuGluLysGluLeuAlaLeuGlu 240

Qy 721 AAGGAAATGCACAGCTGGAAATGGAGTTGCAAGCACTGGAAAGAAAGAACTGGCTCAGGCA 780

Db 241 LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAla 260

Qy 781 GCATCTCAGCCGAGAGGCGCCCAATCAAGCCCTGCTCCATCGCAATGCCAGCACCT 840

Db 261 AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPro 280

Qy 841 AACCTCTTGGGTGACCATCCGCTCTTCATCTTCCTCCAAAGATCAAGGATGTACTCATG 900

Db 281 AsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMet 300

Qy 901 ATCTCCTGAGCCCCATAGTCACATGTGTGGTGTGATGTGAGCGAGGATGACCCAGAT 960

Db 301 IleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAsp 320

Qy 961 GTCCAGATCAGCTGGTTTGTGAACACGCTGGAAGTACACACAGCTCAGACACAAACCCAT 1020

Db 321 ValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHis 340

Qy 1021 AGAGAGGATTACAAACAGTACTCTCCGGGTGGTGTGAGTGTGCTCCCTCCATCCAGCACAGGAC 1080

Db 341 ArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAsp 360

Qy 1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAACAAAGACCTCCAGCGCCCATC 1140

Db 361 TrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIle 380

Qy 1141 GAGAGACCATCTCAAAACCCAAAGGTCAGTAGAGCTCCACAGGTTATATGCTTCGCT 1200

Db 381 GluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPro 400

Qy 1201 CCACCAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTC 1260

Db 401 ProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPhe 420

Qy 1261 ATGCTGGAACACATTTACGTGGAGTGGACCAACACCGGAAACACAGACTAAACTACAAG 1320

Db 421 MetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLys 440

Qy 1321 AACACTGAACAGCTCTGGACTCTGTGTTCTTACTTCTATGTACAGCAAGCTCAGAGTG 1380

Db 441 AsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVal 460

Qy 1381 GAAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTTCAGTGGTCCAGAGGGCTG 1440

Db 461 GluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeu 480

Qy 1441 CACAATCACCACAGCACTAAGAGCTTCTCCGGACTCCGGGT 1482

Db 481 HisAsnHisThrThrLysSerPheSerArgThrProGly 494

RESULT 2

ABB56471

ID ABB56471 standard; protein; 551 AA.

XX AC ABB56471;

XX DT 25-FEB-2002 (first entry)

XX DX

XX DE Murine pCB223 protein.

XX KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis;


```
Db 164 AspValTyrAspCysArgValGluHisTrpGlyLeuAspGluProLeuLeuLysHisTrp 183
QY 616 GAACCTGAGATTCCAGCCCGCCAGTGTGAGCTGACAGAACT--CGAGGTGAGGATCC 672
Db 184 GluPheAspAlaProSerProLeuProGluThrGluValAspGlyGlyGlyGly 203
QY 673 ACTACA-----GCTCCATCAGCTCAGCTCGAAAGAGCTCCAGGCGCTGGAG 720
Db 204 LeuThrAspThrLeuGlnAlaGluThrAspGlnLeuGluAspGlySerAlaLeuGln 223
QY 721 AAGGAAATCCACAGCTGGGAATGGGAGTTCAGACGCTGGAAGAACTG---GCTCAG 777
Db 224 ThrGluIleAlaAsnLeuLysGluLysGluLysLeuGluPheIleLeuAlaHis 243
QY 778 GCAGCATCTGAGCCCGAGGCGCCCAATCAAGCCCTGCTCCATCAAGATGATGACTC 837
Db 244 AlaAlaSerGluProArgGlyProThrIleLysProCysProCysLysCysProAla 263
QY 838 CCTAACCTCTTGGGTGGACCATCCGCTTCTCATCTTCCCTCCAAAGATCAAGATGACTC 897
Db 264 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 283
QY 898 ATGATCTCCTGAGCCCGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 957
Db 284 MetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspPro 303
QY 958 GATGTCCAGATCAGCTGGTTGTGGAACAAGTGAAGTACACAGCTCAGACACAAACC 1017
Db 304 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr 323
QY 1018 CATAGAGAGGATTACACAGTACTCTCCGGGTGGTCTAGTCCCTCCCATCCAGCACAG 1077
Db 324 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 343
QY 1078 GACTGATGAGTGGGAGGAGTTCAAATGCAAGGTCAACAAAGACTCTCCAGCGGCC 1137
Db 344 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro 363
QY 1138 ATCGAGAGAACCTCTCAAAACCAAGGTGAGTCAAGCTCCAGGTATATGCTTG 1197
Db 364 IleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeu 383
QY 1198 CTCCACCAAGAGAGATGACTAAAGAAACAGTCACTCTGACCTGCATGTCACAGAC 1257
Db 384 ProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 403
QY 1258 TTCATGCTGAAGACATTTACGTGGAGTGGACCAACACGGGAAACAGAGCTAAACTAC 1317
Db 404 PheMetProGluAspIleTyrValGluThrAsnAsnGlyLysThrGluLeuAsnTyr 423
QY 1318 AAGAACACTGAACCTGCTGAGTCTGATGTTCTTACTTCTATGTACAGCAGCTGAGA 1377
Db 424 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 443
QY 1378 GTCGAAAAGAACTCGGGTGGGAAAGAAATAGTACTCTCTGTTTCAGTGGTCCACAGGGT 1437
Db 444 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 463
QY 1438 CTGCAAAATCACCACGACTAAGAGCTTCTCCCGGACTCCGGT 1482
Db 464 LeuHisAsnHisThrThrLysSerPheSerArgThrProGly 478
RESULT 4
ABB56461
ID ABB56461 standard; protein; 774 AA.
XX
AC ABB56461;
XX
DT 25-FEB-2002 (first entry)
XX
DE IAS MBP 1-14 CK protein.
XX
```

```
KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
KW antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
KW rheumatoid arthritis; systemic lupus erythematosus.
XX
Mus sp.
OS Synthetic.
PN WO200170245-A1.
XX
27-SEP-2001.
XX
22-MAR-2001; 2001WO-US009616.
XX
22-MAR-2000; 2000US-0191274P.
PR 15-MAY-2000; 2000US-0204249P.
PR 23-JAN-2001; 2001US-0264003P.
XX
(CORI-) CORIXA CORP.
XX
Carter D, Zhu S, Arimilli S, Wang A;
PI
WPI; 2001-616371/71.
DR N-PSDB; ABI99031.
XX
Multimeric complex for treating autoimmune diseases, comprises first and
second single chain MHC class II molecules, each comprising alpha1 and
PT beta1 domain linked through amino acid linker and multimerization domain.
XX
Example 7; Page 105-107; 147pp; English.
XX
The invention relates to a multimeric complex comprising a first
recombinant single chain major histocompatibility complex (MHC) class II
molecule and a second recombinant single chain MHC class II molecule,
each comprising an alpha1 domain and a beta1 domain linked through an
amino acid linker and a multimerization domain. The first and the second
molecule are linked through the multimerization domain to form a
multimeric complex. The complex is useful for treating autoimmune
diseases. It is useful for treating insulin dependent diabetes, multiple
sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
erythematosus. The present sequence is a single chain MHC class II
molecule of the invention
XX
SQ Sequence 774 AA;
Alignment Scores:
Pred. No.: 3,08e-137 Length: 774
Score: 1733.00 Matches: 335
Percent Similarity: 70.71% Conservative: 44
Best Local Similarity: 62.50% Mismatches: 79
Query Match: 64.30% Indels: 78
DB: 4 Gaps: 8
US-10-048-116-1 (1-1484) x ABB56461 (1-774)
QY 64 GSAGGT-----GAAGACGACATTGAGCGCGACGAGCTTCTTGTGTACAACT 114
Db 253 GlyGlySerSerSerGluAspIleGluAlaAepHisValGlyValTyrGlyThrThr 272
QY 115 GTTTATCAGTCTCTGGAGACATTGGCCAGTACACATGAATTTTCATGTTGATGAGTTG 174
Db 273 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrp 292
QY 175 TTCTATGTGGACTTGGATAAGAGAAACTGTCTGGAGGCTTCTCTGAGTTTGGCCAAATTG 234
Db 293 PheTyrValAspLeuAspLysLysGluThrIleTrpMetLeuProGluPheGlyGlnLeu 312
QY 235 ATACTCTTTGAGCCCGCCAGGTGAGTGGAAAACATGCTGCAGAAAACACAACTTGGGA 294
Db 313 ThrSerPheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly 332
```

```
QY 295 ATCTTGACTAAGAGGTCAAAATTTACCCAGCTACCAATGAGGCTCTCTCAGAGCACTGTG 354
Db 333 IleLeuThrLysArgSerThrProAlaThrAsnGluAlaProGlnAlaThrVal 352
QY 355 TTCCCAAGTCCCTGTCTGCTGCTGAGCCCAACACCCCTTATCTGCTTTGTGGCAAC 414
Db 353 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 372
QY 415 ATCTTCCACCTGTGATCAACATCACATGCTGCTCAGAAATAGCAAGTCAGTCACAGAGCGC 474
Db 373 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 392
QY 475 GTTTATGAGACAGCTTCTCTGTCACCCGTGACCATTCCTTCCACAGACTGCTTATCTC 534
Db 393 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 412
QY 535 ACCTTTCATCCCTCTGATGATGACATTTATCAGTCGAAAGTGGAGCACTGGGGCTGGAG 594
Db 413 ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 432
QY 595 GAGCCGGTTCTGAACACTGGAACCTGAGATTCCAGCCCCCATGTCCAGAGCTGCACAGAA 654
Db 433 GluProValLeuLysHisTrp-----Ala 440
QY 655 ACTGAGGTGGAGATCC-----ACTACAGCTCCATCA----- 687
Db 441 SerGlyGlyGlySerGlyGlyGlyAlaLysThrThrProSerValTyrPro 460
QY 687 ----- 687
Db 461 LeuAlaProGlySerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuValLys 480
QY 687 ----- 687
Db 481 GlyTyrPheProGluProValThrValThrTrpAsnSerGlySerLeuSerSerGlyVal 500
QY 688 -----GCTCAGCTCGAAAAGAGCTCCAGGCCCTGGAGAGGAAAATGCA--- 732
Db 501 HisThrPheProAlaValLeuGlnSerAspLeuTyrThrLeuSerSerSerValThrVal 520
QY 733 ---CAGCTGGAATGGAGGTTCCAGCACTGGAAGAACTGGCTCAGGAGCATCTGAG 789
Db 521 ProSerSerThrTrpProSerGluThrValThrCysAsnValAlaHisProAlaSerSer 540
QY 790 CCCAGA---GGGCCCAATCAAGCCC-----TGCTCTCCATGCAAAATGCCCA 834
Db 541 ThrLysValAspLysLysIleValProArgAspCysGlyCysLysProCysIleCysThr 560
QY 835 GCACCTAACCTCTTGGGTGGACCATCGCTCTTCATCTCCCTCCAAAGATCAAGATGTA 894
Db 561 ValProGluVal-----SerSerValPheIlePheProProLysPheLysAspVal 577
QY 895 CTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGATGTGAGCAGGATGAC 954
Db 578 LeuThrIleThrLeuThrProLysValThrCysValValValAspIleSerLysAspAsp 597
QY 955 CCAGATGTCAGATCAGCTGTTGTGAACACCTGGAAGTACACAGCTCAGACACAA 1014
Db 598 ProGluValGlnPheSerTrpPheValAspAspValGluValHisThrAlaGlnThrGln 617
QY 1015 ACCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTTCAGTGCCTCCCATCAGCAC 1074
Db 618 ProArgGluGluGlnPheAsnSerThrPheArgSerValSerGluLeuProIleMetHis 637
QY 1075 CAGGACTGGATGAGTGGCAAGGATTCAAATGCAAGGTCAACAAAGAGCTCCACAGCG 1134
Db 638 GlnAspTrpLeuAsnGlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAla 657
QY 1135 CCCATCGAGAGAACCATCTCAAAACCCCAAGGGTCAGTACAGCTCCACAGGTATATGTC 1194
Db 658 ProIleGluLysThrIleSerLysThrLysGlyArgProLysAlaProGlnValTyrThr 677
```

```
QY 1195 TTGCTCCACAGAGAGAGATGACTAAGAAACAGAGCTCTGACCTGCATGGTCACA 1254
Db 678 IleProProLysGluGlnMetAlaLysAspLysValSerLeuThrCysMetIleThr 697
QY 1255 GACTTTCATGCTTGAAGACATTTACGTGGAGTGGACCAACACGGAACACAGAGCTAAAC 1314
Db 698 AspPhePheProGluAspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGluAsn 717
QY 1315 TACAAGAACTGAAACAGCTCCTGGAGCTCTGATGGTTCTTACTTTCATGTCAGCAAGCTG 1374
Db 718 TyrLysAsnThrGlnProIleMetAspThrAspGlySerTyrPheValTyrSerLysLeu 737
QY 1375 AGAGTGAAGAAAGAACTGGTGGAAAGAAATAGTACTCTCTGTTTCAGTGGTCCAGCAG 1434
Db 738 AsnValGlnLysSerAsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGlu 757
QY 1435 GGTCTGCACAAATCACCACAGCACTAAGAGCTTCTCCCGGACTCCGGGT 1482
Db 758 GlyLeuHisAsnHisThrGluLysSerLeuSerHisSerProGly 773

RESULT 5
ABB56463
ID ABB56463 standard; protein; 772 AA.
AC ABB56463;
XX
XX 25-FEB-2002 (first entry)
XX
XX IAS MBP 90-101 CH1.H.CH2.CH3 protein.
XX
XX Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
XX single chain; immunosuppressive; antidiabetic; antiinflammatory;
XX antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
XX autoimmune disease; insulin dependent diabetes; multiple sclerosis;
XX myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
XX rheumatoid arthritis; systemic lupus erythematosus.
XX
OS Mus sp.
OS Synthetic.
XX
XX WO200170245-A1.
XX
XX 27-SEP-2001.
XX
XX 22-MAR-2001; 2001WO-US009616.
XX
XX 22-MAR-2000; 2000US-0191274P.
XX
XX 15-MAY-2000; 2000US-0204249P.
XX
XX 23-JAN-2001; 2001US-0264003P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Carter D, Zhu S, Arimilli S, Wang A;
XX
XX WPI: 2001-616371/71.
XX
XX N-PSDB; ABI99033.
XX
XX Multimeric complex for treating autoimmune diseases, comprises first and
XX second single chain MHC class II molecules, each comprising alpha and
XX beta domain linked through amino acid linker and multimerization domain.
XX
XX Example 7; Page 109-112; 147pp; English.
XX
XX The invention relates to a multimeric complex comprising a first
XX recombinant single chain major histocompatibility complex (MHC) class II
XX molecule and a second recombinant single chain MHC class II molecule,
XX each comprising an alpha domain and a beta domain linked through an
XX amino acid linker and a multimerisation domain. The first and the second
XX molecule are linked through the multimerisation domain to form a
XX multimeric complex. The complex is useful for treating autoimmune
XX diseases. It is useful for treating insulin dependent diabetes, multiple
XX sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
XX encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
```

erythematous. The present sequence is a single chain MHC class II molecule of the invention

Sequence 772 AA;

Alignment Scores:

Pred. No.:	3,4e-137	Length:	772
Score:	1732.50	Matches:	335
Percent Similarity:	70.58%	Conservative:	44
Best Local Similarity:	62.38%	Mismatches:	79
Query Match:	64.29%	Indels:	79
DB:	4	Gaps:	8

US-10-048-116-1 (1-1484) x AB856463 (1-772)

64	QY	GGAGGT-----GAAGACGACATTTGAGGCGGACACGTAGGCTTCTATGGTACAACT	114
250	Db	GlyGlySerSerSerGluAspAspIleGluAlaAspHisValGlyValTyrGlyThrThr	269
115	QY	GTTTATCAGTCCTCGGACACATTCGGCAGATACACACATGAATTTGATGTGATGAGTTG	174
270	Db	ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrp	289
175	QY	TTCTATGTGGACTTGATTAAGAAGAAAACCTGCTGGAGGCTTCTCGAGTTTGGCCCAATTG	234
290	Db	PheTyrValAspLeuAspIleGlyGlnThrIleTrpMetLeuProGluPheGlyGlnLeu	309
235	QY	ATACTCTTTGAGCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA	294
310	Db	ThrSerPheAspProGlnGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly	329
295	QY	ATCTTGACCTAAGAGGTCAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCAGCTGTG	354
330	Db	IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal	349
355	QY	TTCCCCAAGTCCCTGTGCTGTGGGTGAGGCCCAACACCTTATCTGCTTTGTGGCAAC	414
350	Db	PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn	369
415	QY	ATCTTCCCACTGTGATCAACATCATATGCTGCTCAGAAATAGCAAGTCAGTCACAGCGGC	474
370	Db	IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly	389
475	QY	GTTTATGACACAGCTTCTCGTCAACCGTGACCATTCCTTCCACAGAGCTGCTTATCTC	534
390	Db	ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu	409
535	QY	ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCAGCTGGGCGCTGGAG	594
410	Db	ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu	429
595	QY	GAGCCGGTCTGAACACATGGGAACCTCAGATTCCAGCCCCCATGTCCAGAGCTGCACAGAA	654
430	Db	GluProValLeuLysHisTrp-----Ala	437
655	QY	ACTGGAGGTGGAGGATCC-----ACTACAGCTCCATCA-----	687
438	Db	SerGlyGlyGlyGlySerGlyGlySerLeuAlaLysThrThrProProSerValTyr	457
687	QY	-----	687
458	Db	ProLeuAlaProGlySerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuVal	477
687	QY	-----	687
478	Db	LysGlyTyrPheProGluProValThrValThrTrpAsnSerGlySerLeuSerSerGly	497
688	QY	-----GCTCAGCTCGAAAAAGAGCTCCAGGCCCTCGGAGAAAGGAAAAATGCA	732
498	Db	ValHisThrPheProAlaValLeuGlnSerAspLeuTyrThrLeuSerSerSerValThr	517
733	QY	-----CAGCTGGAATGGAGGTGCAGCACTGGAAAAAGCACTGGCTTCAGGCAGCATCT	786

RESULT 6

ABB56458
ID ABB56458 standard; protein: 676 AA.

AC ABB56458:

DT 25-FEB-2002 (first entry)

DE IAS MBP 1-14 CH1.H protein.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
 single chain; immunosuppressive; antidiabetic; antiinflammatory;
 antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
 autoimmune disease; insulin dependent diabetes; multiple sclerosis;
 myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
 rheumatoid arthritis; systemic lupus erythematosus.

XX
SO
Mus sp.

OS Synthetic.

XX

PN WO200170245-A1.

XX 6

PD 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US009616.
 XX PF
 XX PR
 XX 22-MAR-2000; 2000US-0191274P.
 XX PR
 XX 15-MAY-2000; 2000US-0204249P.
 XX PR
 XX 23-JAN-2001; 2001US-0264003P.
 XX PR
 XX (CORI-) CORIXA CORP.
 XX PA
 XX Carter D, Zhu S, Arimilli S, Wang A;
 XX PI
 XX WPI; 2001-616371/71.
 XX DR
 XX N-PSDB; AS199028.
 XX DR
 XX Multimeric complex for treating autoimmune diseases, comprises first and
 XX PT second single chain MHC class II molecules, each comprising alpha1 and
 XX PT beta1 domain linked through amino acid linker and multimerization domain.
 XX PT
 XX Example 7; Page 99-101; 147pp; English.
 XX PS
 XX The invention relates to a multimeric complex comprising a first
 CC recombinant single chain major histocompatibility complex (MHC) class II
 CC molecule and a second recombinant single chain MHC class II molecule,
 CC each comprising an alpha1 domain and a beta1 domain linked through an
 CC amino acid linker and a multimerization domain. The first and the second
 CC molecule are linked through the multimerization domain to form a
 CC multimeric complex. The complex is useful for treating autoimmune
 CC diseases. It is useful for treating insulin dependent diabetes, multiple
 CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
 CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
 CC erythematosus. The present sequence is a single chain MHC class II
 CC molecule of the invention
 XX SQ

Sequence 676 AA;

Alignment Scores:

Pred. No.:	2,396-119	Length:	676
Score:	1521.00	Matches:	304
Percent Similarity:	71.98%	Conservative:	12
Best Local Similarity:	69.25%	Mismatches:	39
Query Match:	56.44%	Indels:	84
DB:	4	Gaps:	8

US-10-048-116-1 (1-1484) x ABB56458 (1-676)

Qy	64	GGAGGT-----	GAAGACGACATTGAGCCGACACCGTAGGCTTCTATGTGTACAACT	114
Db	250	GlyGlySerSerSerGluAspIleGluAlaAspHisValGlyValTyrGlyThrThr		269
Qy	115	GTTTATCATGCTCTCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGAGTTG		174
Db	270	ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrp		289
Qy	175	TTCTATGTGGACTGGTAAGAAACTCTCTGGAGGCTCTCTGAGTTTGGCAATTG		234
Db	290	PheTyrValAspLeuAspLysGlyGlnThrIleTrpMetLeuProGluPheGlyGlnLeu		309
Qy	235	ATACTCTTTGAGCCCCAGGTGGAGTGCAAAACATAGCTGCAGAAAAACACAACTTGGGA		294
Db	310	ThrSerPheAspProGlnGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly		329
Qy	295	ATCTTGACTAAGAGTCAAAATTTACCCCGCTACCAATGAGGCTCTCAAGGACTGTG		354
Db	330	IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal		349
Qy	355	TTCCCCAGTCCCTGTGCTGCTGGTCAGCCCAACACCTTATCTGCTTGTGTGCAAC		414
Db	350	PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn		369
Qy	415	ATCTTCCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGCGGC		474
Db	370	IlePheProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly		389

Qy	475	GTTTATGAGACCGACTTCCTCGTCAACCGTGACCACTTCCTTCCACAAGCTGTCTTATCTC	534
Db	390	ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu	409
Qy	535	ACTTTCATCCTCTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAG	594
Db	410	ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu	429
Qy	595	GAGCCGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTGACAGCTGACAGAA	654
Db	430	GluProValLeuLysHisTrp-----	Ala 437
Qy	655	ACTGGAGGTGAGGATCC-----	ACTACAGCTCCATCA- 687
Db	438	SerGlyGlyGlySerGlyGlyGlyAlaLysThrThrProProSerValTyrPro	457
Qy	687	-----	687
Db	458	LeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLys	477
Qy	687	-----	687
Db	478	GlyTyrPheProGluSerValThrValThrTrpAsnSerGlySerLeuSerSerSerVal	497
Qy	688	-----	732
Db	498	HisThrPheProAlaLeuGlnSerGlyLeuTyrThrMetSerSerSerValThrVal	517
Qy	733	---CAGCTGGAATGGGAGTTGCAAGCACTGGAAGAACTGGCTCAGCGAGCATCT---	786
Db	518	ProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHisProAlaSerSer	537
Qy	787	-----	819
Db	538	ThrThrValAspLysLysLeuGluProSerGlyProIleSerThrIleAsnProCysPro	557
Qy	820	CCATGC-----	867
Db	558	ProCysLysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPhe	577
Qy	868	ATCTTCTCCTCAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGT	927
Db	578	IlePheProProAsnIleLysAspValLeuMetIleSerLeuThrProLysValThrCys	597
Qy	928	GTGTGTGTGATGTGACGAGGATGACCCAGATGTCCAGATCAGCTGTTTGTGAACAAC	987
Db	598	ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn	617
Qy	988	GTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCGG	1047
Db	618	ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArg	637
Qy	1048	GTGTGTGATGCTCCCTCCATCCAGCACAGACTGGATGATGGCAAGGATTCAAAATGC	1107
Db	638	ValValSerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys	657
Qy	1108	AAGTCAACAACAAGACCTCCCGAGCCCCCATCGAGAGAACCATCTCAAAACCCAAA	1164
Db	658	LysValAsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLys	676

RESULT 7

ABB56457
 ID ABB56457 standard; protein; 678 AA.

XX AC ABB56457;

XX DT 25-FEB-2002 (first entry)

XX DE IAS MBP 1-14 CH1.H.CH2.CH3 protein.

XX KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
 KW single chain; immunosuppressive; antidiabetic; antiinflammatory;
 KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;

KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;
 KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
 KW rheumatoid arthritis; systemic lupus erythematosus.

OS Mus sp.
 OS Synthetic.

XX WO200170245-A1.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US009616.

XX 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.

PR 23-JAN-2001; 2001US-0264003P.

PA (CORI-) CORIXA CORP.

XX Carter D, Zhu S, Arimilli S, Wang A;

XX WPI; 2001-616371/71.

XX N-PSDB; ABI99027.

PT Multimeric complex for treating autoimmune diseases, comprises first and

PT second single chain MHC class II molecules, each comprising alpha1 and

PT beta1 domain linked through amino acid linker and multimerization domain.

XX Example 7; Page 96-98; 147pp; English.

XX The invention relates to a multimeric complex comprising a first
 CC recombinant single chain major histocompatibility complex (MHC) class II
 CC molecule and a second recombinant single chain MHC class II molecule,
 CC each comprising an alpha1 domain and a beta1 domain linked through an
 CC amino acid linker and a multimerization domain. The first and the second
 CC molecule are linked through the multimerization domain to form a
 CC multimeric complex. The complex is useful for treating autoimmune
 CC diseases. It is useful for treating insulin dependent diabetes, multiple
 CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
 CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
 CC erythematosus. The present sequence is a single chain MHC class II
 CC molecule of the invention

XX Sequence 678 AA;

Alignment Scores:

Pred. No.: 2.39e-119 Length: 678
 Score: 1521.00 Matches: 304
 Percent Similarity: 71.98% Conservative: 12
 Best Local Similarity: 69.25% Mismatches: 39
 Query Match: 56.44% Indels: 84
 DB: 4 Gaps: 8

US-10-048-116-1 (1-1484) x ABB56457 (1-678)

QY 64 GGAGGT-----GAAGACGACATTGAGCGCCAGCCAGCTAGGCTTCTATGTACAACT 114
 DB 252 GLVGLYSerSerSerGluAspAspIleGluAlaAspHisValGlyValTyrGlyThrThr 271
 QY 115 GTTTATCAGTCTCTGAGACATTGGCCAGCTACACATCAATTTGATGGTGTGATGTTG 174
 DB 272 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyr 291
 QY 175 TTCTATGTGACATTGGNTAGAGAAAACCTGTCTGGAGGCTTCTGAGTTTGGCCAAATG 234
 DB 292 PheTyrValAspLeuAspLysLysGluThrIleTyrMetLeuProGluPheGlyGlnLeu 311
 QY 235 ATACTCTTTCAGCCCAAGGTGGACTGCAAAACATAGCTCCAGAAAACACAACTTTGGGA 294
 DB 312 ThrSerPheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly 331
 QY 295 ATCTTGACTAAGAGGTCAAAATTTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCGACTGTG 354
 |||||||

Db 332 IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal 351
 QY 355 TTCCCAAGTCCCTCTGCTGCTGGGTGAGCCCAACACACCTTATCTGCTTTGGGCAAC 414
 Db 352 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 371
 QY 415 ATCTTCCCACTCTGTGATCAACATCAGCTGCTCAGAAATAGCAAGTCAGTCACAGCGGC 474
 Db 372 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 391
 QY 475 GTTTATGAGACGAGCTTCTCTGCTCAACCGTGACCATCTCTTCCACAGCTGTCTTATCTC 534
 Db 392 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 411
 QY 535 ACCTTCATCCCTCTCATGATGATGATTTATGCTGCAAGGTGAGCACTGGGCGCTGGAG 594
 Db 412 ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 431
 QY 595 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCTCAGAGCTGACAGAA 654
 Db 432 GluProValLeuLysHisTrp-----Ala 439
 QY 655 ACTGGAGGTGGAGGATCC-----ACTACAGCTCATCA----- 687
 Db 440 SerGlyGlyGlySerGlyGlyAlaLysThrThrProSerValTyrPro 459
 QY 687 ----- 687
 Db 460 LeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLys 479
 QY 687 ----- 687
 Db 480 GlyTyrPheProGluSerValThrValThrTrpAsnSerGlySerLeuSerSerVal 499
 QY 688 -----GCTCAGCTCGAAAAGAGCTCCAGGCCCTGGAGGAAGAAATGCA--- 732
 Db 500 HisThrPheProAlaLeuLeuGlnSerGlyLeuTyrThrMetSerSerValThrVal 519
 QY 733 ---CAGCTGGAATGGAGTTGCAAGCACTGGAAGAACTGGCTCAGGCGAGCATCT--- 786
 Db 520 ProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHisProAlaSerSer 539
 QY 787 -----GAGCCCGAGAGGGCCC-----ACAATCAAGCCCTGTCTCT 819
 Db 540 ThrThrValAspLysLysLeuGluProSerGlyProIleSerThrIleAsnProCysPro 559
 QY 820 CCATGC-----AAATGCCCGAGCACCTTAACCTCTTGGGTGGAGCATCCGTCTTC 867
 Db 560 ProCysLysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPhe 579
 QY 868 ATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGT 927
 Db 580 IlePheProProAsnIleLysAspValLeuMetIleSerLeuThrProLysValThrCys 599
 QY 928 GTGGTGGTGGATGTGAGCGAGGATGACCCAGAGATGTCAGATCAGCTGGTGTGTGAACAAC 987
 Db 600 ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn 619
 QY 988 GTGGAAAGTACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGG 1047
 Db 620 ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArg 639
 QY 1048 GTGGTCAAGTCCCTCCCATCCAGCACAGGATGGATGAGTGGCGAGGATTCATCAATGC 1107
 Db 640 ValValSerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys 659
 QY 1108 AAGGTCAACAAACAAAGACCTCCAGCGCCCATCCAGAGAACCATCTCAAAACCCCAA 1164
 Db 660 LysValAsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLys 678
 |||||||

RESULT 8
 ADL15170
 ID ADL15170 standard; protein; 426 AA.

XX	ADL15170;	Db	102	-----ProSerValTyrProLeuAlaProGlySerAlaAlaGln	114
AC					
XX					
DT	06-MAY-2004 (first entry)	Qy	385	CCCAACACCCCTTATC-----TGCTTTGTGGCAACATCTTCCACCTGTGATCAAC	435
XX					
DE		Db	115	ThrAsnSerMetValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr	134
XX					
XX					
KW	Modified S immunoglobulin antibody; constant region; immunoglobulin; Ig;	Qy	436	ATCATAGCTGCTCAAAATAGCAAGTCACTGACACACGGCGTTTATGAGACAGCTTCTC	495
KW	IgG2a; modified S antibody; S-Ab; immune disorder; infectious disorder;				
KW	cancerous disorder; murine; antirheumatic; antiarthritic; osteopathic;	Db	135	ValThrTrp-----AsnSerGlySerLeuSerGlyValHisThrPheProAlaVal	152
KW	antiinflammatory; dermatological; immunosuppressive; ophthalmological;				
KW	antibacterial; virucide; anti-HIV; vasotropic; antiallergic;	Qy	496	GTCAACCGTGACCATCTCTCCCAAGCTGTCTTATCTCACCTTCTCCTCTCTGAT---	552
KW	hepatotropic.				
XX		Db	153	LeuGluSerAsp-----LeuTyrThrLeuSerSerSerValThrValProSerSerPro	170
OS	Mus sp.				
XX					
XX		Qy	553	-----GATGACATTTATGACTGCAAGGTGGAGCAGCTGGGGCCTGGAGGACCGGTTCTG	606
PN	US2003232046-A1.				
XX		Db	171	ArgProSerGluThrValThrCysAsnValAlaHis-----	182
XX					
PD	18-DEC-2003.				
XX		Qy	607	AAACACTGGGAACCTGAGATTCCAGCCCCCATGTACAGCTGACAGAAACTGGAGGTGGA	666
PF	05-JUN-2003; 2003US-00454948.				
XX		Db	182	-----	182
PR	14-JUN-2002; 2002US-0388896P.				
XX		Qy	667	GGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAA	726
XX	(SCAL/) SCALLON B J.				
PA	(CAIA/) CAI A.	Db	183	-----ProAlaSerSerThrLysValAspLysLysile-----	193
PA	(NASO/) NASO M.				
XX		Qy	727	AATGCACAGCTGGGAATGGGAGTTGCAAGCACTGGAAAAAGAACTGGCTCAGGCAGCATCT	786
XX	Scallon BJ, Cai A, Naso M;				
PI		Db	193	-----	193
XX	WPI; 2004-052145/05.				
DR		Qy	787	GAGCCAGAGGGCCCAACAATCAAGCCCTGTCTCCATGCAAAATGCCAGACCTTAACCTC	846
XX					
PT	Modified S immunoglobulin molecule useful for treating immune disorder or	Db	194	GluProArgGlyProThrIleLysProCysProCysLysCysProAlaProAsnLeu	213
PT	diseases especially immune conditions e.g. rheumatoid arthritis,				
PT	osteoarthritis, inflammatory bowel disease or systematic lupus	Qy	847	TTGGGTGGACCATCCGCTTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATCATCTCC	906
PT	erythematosus.				
XX		Db	214	LeuGlyGlyProSerValPheIlePheProLysIleLysValLeuMetIleSer	233
PS	Example 1; SEQ ID NO 2; 37pp; English.				
XX		Qy	907	CTGAGCCCCATAGTCACATGTGTGGTGGTGTGAGCGAGGATGACCCAGATGTCCAG	966
CC	The present invention relates to modified "s" immunoglobulin antibodies				
CC	that have an extra constant region immunoglobulin (Ig) domain inserted	Db	234	LeuSerProIleValThrCysValValValSerValSerGluAspAspProAspValGln	253
CC	into the constant region of the Ig molecule. Preferably, the extra				
CC	constant region Ig domain comprises a CH3, CH1 or CH2 domain, and the Ig	Qy	967	ATCAGCTGGTGTGGAACAGCTGGAGTGAACACAGCTCAGACACAAACCCATAGAGAG	1026
CC	molecule is IgG1, where the extra constant region Ig domain comprises a				
CC	CH1 domain of an IgG2a immunoglobulin. The modified "s" antibody (S-Ab)	Db	254	IleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGlu	273
CC	is useful for treating immune disorders (e.g. rheumatoid				
CC	arthritis/seronegative arthropathies, osteoarthritis, inflammatory bowel	Qy	1027	GATTACAACAGTAGTCTCTCCGGGTGGTCAAGTCCCTCCCATCCAGCACACAGGATGGATG	1086
CC	disease, systematic lupus erythematosus, iridocyclitis/uvetis/optic				
CC	neuritis, idiopathic pulmonary fibrosis, systemic vasculitis/wegener's	Db	274	AspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMet	293
CC	granulomatosis), and infectious or cancerous disorders (e.g. chronic				
CC	bacterial infection, acute and chronic parasitic or infectious processes,	Qy	1087	AGTGGCAAGGAGTTCAAAATGCAAGGTCAACAAACAAAGACTTCCAGCGCCCATCGAGAGA	1146
CC	including bacterial, viral and fungal infections, HIV infection/HIV				
CC	neuropathy, meningitis, hepatitis, septic arthritis, peritonitis,	Db	294	SetGlyLysGluPheLysCysLysValAsnLysAspLeuProAlaProIleGluArg	313
CC	pneumonia, epiglottitis).				
CC	The present sequence represents a murine S-Ab	Qy	1147	ACCATCTCAAAACCCCAAGGGTCAAGTGAAGCTCCAGAGTATATGTCTGCCTCCACCA	1206
XX					
SQ	Sequence 426 AA;	Db	314	ThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuProProPro	333
		Qy	1207	GAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGTCATGGTCACAGACTTCATGCCT	1266
		Db	334	GluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetPro	353
		Qy	1267	GAAGACATTTACGTGGAGTGGACCAACACCGGAAAAACAGAGCTAAACTCAAGAACACT	1346
		Db	354	GluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThr	373
		Qy	1327	GAACCACTCTGGACTGATGGTTCTTACTTCACTGACAGCAGCTGAGAGTGGAAAG	1386
		Db	374	GluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLys	393
		Qy	1387	AAGAACTGGGTGGAAAAAAGAAATAGTACTCTCTGTTCAGTGGTCCACGAGGCTCTCA	1446

Alignment Scores:

Pred. No.:	5e-103	Length:	426
Score:	1327.00	Matches:	264
Percent Similarity:	70.15%	Conservative:	25
Best Local Similarity:	64.08%	Mismatches:	49
Query Match:	49.24%	Indels:	74
DB:	8	Gaps:	7

US-10-048-116-1 (1-1484) x ADL15170 (1-426)

Qy	265	AACATAGCTGAGAAAAACACAACTGGGAATCTTGACTAGAGGTCAAAATTCACCCCA	324
Db	82	AsnValAlaHisProAlaSerSerThrLysValAspLysLysIleAlaLysThrPro	101
Qy	325	GCTACCAATGAGGCTCCTCAAGCAGACTGTGTTCCTCCCAAGTCCCTCTGCTCTGGGTGAG	384

Db 394 LysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsn 413

QY 1447 CACCACAGCACTAAGAGCTTCTCCGGACTCCGGGT 1482

Db 414 HisHisThrThrLysSerPheSerArgThrProGly 425

RESULT 9

AA40384

ID AAR40384 standard; protein; 469 AA.

XX AAR40384;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 08-FEB-1994 (first entry)

XX Monoclonal antibody M(alpha)2-3 Heavy-chain.

XX anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin;

KW bispecific bivalent antibody; cell-targetting; cytotoxic agent.

XX Unidentified.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Region /label= signal_peptide

FT Region 20..139

FT Region /label= variable

FT Region 140..236

FT Region /label= constant

FT Region 237..252

FT Region /label= joining

FT Region 253..362

FT Region /label= constant

FT Region 363..469

FT /label= constant

XX EP556111-A1.

PN 18-AUG-1993.

PD 09-FEB-1993; 93BP-00400323.

PF 11-FEB-1992; 92FR-00001505.

PR (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PA Boulain J, Ducancel F, Gillet D, Menez A;

PI WPI; 1993-260351/33.

XX N-PSDB; AAQ48037.

DR New immunoglobulin hybrid proteins - with immunoglobulin fragments linked

PT to dimeric protein, for diagnostic or therapeutic use.

XX Example 1; Fig 3A; 37pp; French.

XX A fragment of the heavy chain (VH + CH1) from the anti-snake small

CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from

CC hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain

CC fragment (VL + CL) was amplified from the same source using primers

CC AAQ48041 and AAQ48042. The two amplified fragments were inserted into the

CC same vector; the H-chain fragment was inserted (in-frame) between codons

CC 6-7 of the phoA coding sequence and the L-chain fragment was inserted

CC into a cassette which contained a phoA S-D sequence, a signal peptide and

CC the first 6 codons of phoA. The cassette was positioned between the

CC termination codon and the transcription termination sequence of phoA. The

CC fusion construct is expected to encode a hybrid protein comprising two

CC identical Ab-derived units. The invention also covers hybrid proteins

CC containing two different Ab-derived units (i.e. to produce bispecific

CC antibodies). When a toxic protein is used in place of phoA, the hybrid

CC molecules can be used as cell-targetting therapeutic agents. (Updated on

CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct

CC PN field.)

XX SQ Sequence 469 AA;

Alignment Scores:

Pred. No.: 2,22e-102 Length: 469

Score: 1319.50 Matches: 283

Percent Similarity: 60.96% Conservative: 23

Best Local Similarity: 56.37% Mismatches: 71

Query Match: 48.96% Indels: 125

DB: 2 Gaps: 13

US-10-048-116-1 (1-1484) x AAR40384 (1-469)

QY 100 TTCTATGGTACAACTGTTTATCAGTCTCTCTGGAGAC-----ATTGCG----- 141

Db 51 TyrTyrIleAsnTrpValLysGlnLysProGlyGlnGlyLeuLysTrpIleGlyTrpIle 70

QY 142 -----CAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

Db 71 TyrProAlaSerGlyAsnThrLysTyrAsnGluAsnPheLysGlyLysAlaThrLeuThr 90

QY 181 GTGGACTTGGATAAGAGAAACTGCTCGAGGCTTCCTGAGTTT----- 225

Db 91 ValAspThrSerSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSerGluAspThr 110

QY 226 -----GGCCAAATTGATCTCTTTGAGCCC 249

Db 111 AlaValTyrPheCysAlaArgAlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGly 130

QY 250 CAAGTGGAGTCGAAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGAGG 309

Db 131 GlnGlyThrThrLeuThrValSerSerAlaLys----- 141

QY 310 TCAAAATTTCCACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCTCCCAAGTCCCT 369

Db 142 -----ThrThrAlaPro-----SerValTyrProLeuAlaPro 152

QY 370 GTG-----CTGCTGGGTGAGCCCAACACCTTATCTGCTTTCTGTCGACACATCTTC 420

Db 153 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 172

QY 421 CCACCTGTGATCAACATCATCGGTTCGAAATAGCAAGTCAGTCACAGACGCGTTTAT 480

Db 173 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 189

QY 481 GAGACGAGCTTCTCTGTCACCGTGACCATTCCTTCCACAGCTGTCTTATCTCACCTTC 540

Db 190 -----HisThrPheProAlaVal----- 195

QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGTGGAGCACTGGGGCCTGGAGAGCCG 600

Db 196 -----LeuGlnSerAspLeuTyrThrLeuSer----- 204

QY 601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

Db 205 -----SerSerValThrValThr--- 210

QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGTCGAAAAAGAGAGCTCCAGGCCCTGGAG 720

Db 211 -----SerSerThr----- 213

QY 721 AAGGAAATGTCACAGCTGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA 780

Db 214 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 226

QY 781 GCATCT-----GAGCCAGAGGGCCCAACAATCAAGCCCTGT 816

Db 227 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 246

QY 817 CTTCAATGCAATGCCAGCACCTAACCTCTTGGTGGAGACCATCCGCTCTTCATCTCCCT 876

Db 247 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 266

QY	877	CCAAAGATCAGGATGTACTATGATCTCCCTGAGCCCAATAGTCACATGTGTGGTGTG	936
Db	267	ProlysiLeLysAspValLeuMetileSerLeuSerProileValThrCysValValVal	286
QY	937	GATGTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA	996
Db	287	AspValSerGluAspPronaspValGlnileSerTrpPheValAsnValGluVal	306
QY	997	CACAGCTCAGACACAAACCCATAGAGAGATTACAAAGTACTCTCCGGGTGGTCAGT	1056
Db	307	HistThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer	326
QY	1057	GCCTCCCTCCACAGACACAGACTGGATGATGGCAAGAGATTCAATGCAAGGTCAAC	1116
Db	327	AlaLeuProileGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn	346
QY	1117	AACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGCTCAGTAAGA	1176
Db	347	AsnLysAspLeuProAlaProileGluArgThrileSerLysProLysGlySerValArg	366
QY	1177	GCTCCACAGGTATATGTTCTTCCTCCACCAGAGAAGATGACTAAGAAAACAGGTCACT	1236
Db	367	AlaProGlnValTyrValLeuProProGluGluMetThrLysLysGlnValThr	386
QY	1237	CTGACCTCGATGTCACAGACTTCATGCTGAAGACATTTACGTGGAGTGACCAACAC	1296
Db	387	LeuthrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn	406
QY	1297	GGGAAAACAGAGCTAAACTACAAGAACACTGAACAGCTCCGTGGACTCTGATGGTCTTAC	1356
Db	407	GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr	426
QY	1357	TTCATGTACAGACAGCTGAGAGTGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCC	1416
Db	427	PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluAUGAsnSerTyrSer	446
QY	1417	TGTTCAAGTGGTCCAGAGGGTCTGCAATACACACAGACTAGAGAGTTCTCCGGACT	1476
Db	447	CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThr	466
QY	1477	CCGGGT 1482	
Db	467	ProGly 468	
RESULT 10			
AAR13061			
ID	AAR13061 standard; protein; 468 AA.		
XX	AC AAR13061;		
XX	25-MAR-2003 (revised)		
DT	03-OCT-1991 (first entry)		
XX	Monoclonal antibody OK3T heavy chain.		
DE	OK3T; light chain; humanised antibodies; CDR-grafting.		
XX	Mus musculus.		
OS	Key Location/Qualifiers		
XX	Peptide 1..19		
FT	/label= signal peptide		
FT	Protein 20..468		
FT	/label= light chain		
XX	W09109967-A.		
PN	11-JUL-1991.		
XX	21-DEC-1989; 89GB-00028874.		
PF	21-DEC-1989; 89GB-00028874.		
XX			

PR	21-DEC-1990;	90WO-GB002017.
XX	(CLLT) CELLTECH LTD.	
XX	Adair JR, Athwal DS, Emtage JS;	
PI	WPI; 1991-222915/30.	
DR	N-PSDB; AAQ12637.	
XX	New humanised antibodies comprising CDR grafted antibody - with heavy and	
PT	light chains, for use in vivo therapy and diagnosis.	
PT	Disclosure; Fig 2b; 91pp; English.	
XX	The OK3T heavy chain sequence was deduced from the cDNA sequence isolated	
CC	from a library prepared from OK3T producing cells. The library was	
CC	screened with a probe complementary to a region in the mouse IgG2a	
CC	constant domain region. The OK3T sequence was used in CDR-grafting	
CC	experiments to prepare humanised antibodies. (Updated on 25-MAR-2003 to	
CC	correct PA field.)	
XX	SQ Sequence 468 AA;	
XX	Alignment Scores:	
Pred. No.:	7.13e-102	Length: 468
Score:	1313.50	Matches: 265
Percent Similarity:	70.65%	Conservative: 19
Best Local Similarity:	65.92%	Mismatches: 41
Query Match:	48.74%	Indels: 77
DB:	2	Gaps: 8
US-10-048-116-1 (1-1484) x AAR13061 (1-468)		
Qy	310	TCAAATTTCACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCTCCCAAGTCCCTC 369
Db	132	ThrThrLeuThrValSerSerAlaLysThrThrAlaProSerValTyrProLeuAlaPro 151
Qy	370	GTG-----CTGCTGGGTGACGCCAAACACCTTATCTGCTTTGTGGCAACATCTTC 420
Db	152	ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 171
Qy	421	CCACCTGTGATCAACATCATGCTCAGAAATAGCAAGTCAGTCACAGAGCGGTTTAT 480
Db	172	ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 188
Qy	481	GAGACCACTTCCTCGTCAACCGTGACCATTCCTCCCAAGCTGTCTTATCTCACCTTC 540
Db	189	-----HisThrPheProAlaVal----- 194
Qy	541	ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGGACCG 600
Db	195	-----LeuGlnSerAspLeuTyrThrLeuSer----- 203
Qy	601	GTTCTGAAACACTGGGAACCTGAGATTCAGCCCCCATGTGCAGAGCTGCAGAAACTGGA 660
Db	204	-----SerSerValThrValThr--- 209
Qy	661	GGTGGAGGATCCACTACAGCTCCATCATGCTCGAAGAGAGAGCTCCAGGCCCTGGAG 720
Db	210	-----SerSerThr----- 212
Qy	721	AAGGAAATGCACAGCTGGGAATGGAGTTGCNAGCACTGGAAAGGAAGTGGCTCAGGCA 780
Db	213	-----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 225
Qy	781	GCATCT-----GAGCCACAGAGGCCCAACAATCAAGCCCTGT 816
Db	226	AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 245
Qy	817	CCTCATGCAAAATGCCAGACCTTAACCTCTTGGGTGGACCATCCGCTCTCATCTTCCCT 876
Db	246	ProProCysLysCysProAlaProAsnLeuGlyGlyProSerValPheIlePhePro 265

Db 266 ProlysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 285
Qy 937 GATGTGACGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACAGTGGAAAGTA 996
Db 286 AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal 305
Qy 997 CACACAGCTCAGACACAAACCATAGAGAGATTACACAGTACTCTCCGGTGGTCACT 1056
Db 306 HisThrAlaGlnThrGlnThrHisArgGluAspTrpAsnSerThrLeuArgValValSer 325
Qy 1057 GCCCTCCCATCCAGCACAGGATGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1116
Db 326 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 345
Qy 1117 AACAAAGACCTCCAGGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA 1176
Db 346 AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 365
Qy 1177 GCTCCACAGGTATATGCTTGCCTCCACAGAGAGATGACTAAGAACAGGTCACT 1236
Db 366 AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr 385
Qy 1237 CTGACCTGCATGGTCACAGACTTCATGCTCAAGACATTTACGTGGAGTGGACCAACAAC 1296
Db 386 LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn 405
Qy 1297 GGGAAACAGAGCTAAACTACAAGAACACTGAACAGCTCTGGACTCTGATGGTCTTAC 1356
Db 406 GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr 425
Qy 1357 TTCATGTACAGCAAGCTGAGAGTGGMAAGAGAACTGGGTGGAAAGAAATAGTACTCC 1416
Db 426 PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer 445
Qy 1417 TGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACAGCTAAGAGCTTCTCCCGGACT 1476
Db 446 CysSerValValHisGluGlyLeuHisAsnHisIleThrThrLysSerPheSerArgThr 465
Qy 1477 CCGGGT 1482
Db 466 ProGly 467
RESULT 12
ID ADL15695 standard; protein; 329 AA.
AC ADL15695;
XX XX
DT 20-MAY-2004 (first entry)
DE Murine immunoglobulin heavy chain constant region protein SeqID 69.
XX XX
KW mouse; murine; antibody; beta-amyloid; A-beta;
KW amyloid beta A4 precursor protein; APP; presenilin;
KW lipoprotein receptor related protein; LRP; beta-amyloid 42; A-beta 42;
KW Alzheimer's disease; neuroprotective; nontropic.
XX XX
OS Mus musculus.
XX XX
PN WO2004018997-A2.
XX XX
PD 04-MAR-2004.
XX XX
PF 20-AUG-2003; 2003WO-US026173.
XX XX
PR 20-AUG-2002; 2002US-0405417P.
XX XX
PR 18-SEP-2002; 2002US-0411974P.
XX XX
PA (NEUR-) NEUROGENETICS INC.
XX XX
PI Kounnas M, Patrick A, Velicelebi G, Wagner S;
XX XX
XX WPI; 2004-226902/21.
DR

DR N-PSDB; ADL15694.
XX XX
PT New polypeptide comprises a sequence of amino acids that is selectively
PT reactive with beta-amyloid peptide 42 or at least one complementarity-
PT determining region of antibody A387 or B436, useful for treating
PT Alzheimer's disease.
XX XX
PS Claim 35; SEQ ID NO 69; 408pp; English.
XX XX
CC This invention relates to novel methods and compositions for detecting
CC and modulating beta-amyloid (A-beta) peptide levels and the processing of
CC amyloid beta A4 precursor protein (APP). Specifically, it refers to
CC methods of assessing the presenilin activity of compounds using the
CC lipoprotein receptor related protein (LRP), in order to identify
CC presenilin proteins that can be used to affect the processing of APP. The
CC present invention describes methods to identify agents that modulate
CC presenilin activity and A-beta levels, in particular beta-amyloid 42 (A-
CC beta 42), such that the agent is selectively reactive with A-beta 42 and
CC binds at least one complementarity determining region (CDR) of either
CC antibody A387 or antibody B436. As such, the polypeptides, nucleic acids
CC and antibodies are useful for treating Alzheimer's disease, accordingly
CC the compositions exhibit neuroprotective and nontropic activities. This
CC peptide sequence is a murine antibody chain peptide of the invention.
XX XX
SQ Sequence 329 AA;
Alignment Scores:
Pred. No.: 9.37e-102 Length: 329
Score: 1311.50 Matches: 264
Percent Similarity: 71.72% Conservative: 15
Best Local Similarity: 67.87% Mismatches: 33
Query Match: 48.66% Indels: 77
DB: 8 Gaps: 8
US-10-048-116-1 (1-1484) x ADL15695 (1-329)
Qy 349 ACTGTGTTCCTCCCAAGTCCCTGTG-----CTGCTGGTCCAGCCCAACACCTTATC 399
Db 6 SerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSerValThrLeuGly 25
Qy 400 TGCTTTGTGGACAACATCTTCCCACTGTGTCATCAATCAATCACTGGCTCAGAAATAGCAAG 459
Db 26 CysLeuValLysGlyTyrPheProGluProValThrLeuThrTrp-----AsnSerGly 43
Qy 460 TCAGTCAACAGACGCGGTTTATAGACACAGCTTCTCTCAACCGTAGCACTTCCTTCCAC 519
Db 44 SerLeuSerSerGlyVal-----HisThrPhePro 53
Qy 520 AAGCTGTCTTATCTCACCTTCATCCCTTCTGTATGATGATGACATTTATGACTGCAGGTGGAG 579
Db 54 AlaVal-----LeuGlnSerAspLeuTyrThrLeuSer----- 64
Qy 580 CACTGGGGCTGGAGGAGCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATG 639
Db 64 ----- 64
Qy 640 TCAGAGCTGACAGAAACTGGAGTGGAGATTCACACTACAGCTCCATCAGCTCAGCTCGAA 699
Db 65 SerSerValThrValThr-----SerSerThr----- 73
Qy 700 AAAGAGCTCCAGGCCCTGGAGAGAGAAATGCACAGCTGGGAATGGGAGTTGCAAGCACTG 759
Db 74 -----TrpProSerGlnSerIle 79
Qy 760 GAAAAGGAAGTGGCTCAGGCAGCATCT-----GAGCCCAAGA 795
Db 80 ThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGluProArg 99
Qy 796 GGGCCCAATCAAGCCCTCTCTCCATGCAATGCAAGTCCAGCACTAATCTTGGGTGGGA 855
Db 100 GlyProThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGlyGly 119
Qy 856 CCATCCGTCTTCATCTCTCCCTCCCAAGATCAAGATGATCTCATGATCTCCCTGAGCCCC 915

Db 120 ProSerValPheIlePheProLysIleLysAspValLeuMetIleSerLeuSerPro 139
QY 916 ATAGTCACATGTGTGGTGGATGTGAGCGAGATGACCCAGATGTCCAGATCAGCTGG 975
Db 140 IleValThrCysValValValAspValSerGluAspProAspValGlnIleSerTrp 159
QY 976 TTTGTGAACAACTGGAAGTACACAGCTCAGACACAAACCCATAGAGAGGATTACAAC 1035
Db 160 PheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsn 179
QY 1036 AGTACTCTCGGGTGTGCTAGTGCCTCCCTCCATCCAGCACAGACTGGATGAGTGCAG 1095
Db 180 SerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLys 199
QY 1096 GAGTTCAAATGCAAGTCAACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCA 1155
Db 200 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSer 219
QY 1156 AAACCCAAAGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCTCCACAGAAAGAG 1215
Db 220 LysProLysGlySerValArgAlaProGlnValTy-ValLeuProProGluGluGlu 239
QY 1216 ATGACTAAGAAACAGTCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1275
Db 240 MetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIle 259
QY 1276 TAGCTGGAGTGGACCAACAGCGGAAACAGAGCTAACTACAGAACACTGAACACAGTC 1335
Db 260 TyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProVal 279
QY 1336 CTGGACTCTGATGTTCTTACTTCTATCATGTACAGCAAGCTGAGAGTGGAAAGAACTGG 1395
Db 280 LeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrp 299
QY 1396 GTGGAAGAAATAGTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1455
Db 300 ValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisThr 319
QY 1456 ACTAAGAGCTTCTCCCGGACTCCGGGT 1482
Db 320 ThrLysSerPheSerArgThrProGly 328
RESULT 13
ID AAR47450
XX AAR47450 standard; protein; 477 AA.
AC AAR47450;
XX
XX 25-MAR-2003 (revised).
DT 24-JUN-1994 (first entry)
DE T84.12 Heavy chain.
XX Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region;
KW transform; myeloma cell; light chain; tumour.
XX Synthetic.
OS
XX
XX WO9325237-A1.
PN
XX 23-DEC-1993.
XX
XX 15-JUN-1993; 93WO-US005709.
XX
XX 15-JUN-1992; 92US-00904074.
PR
XX (YANG/) YANG Y.
PA (CITY) CITY OF HOPE.
XX
XX Shively JE, Fischer R, Wu A, Paxton R, Yang YH;
PI WPI; 1994-007204/01.
XX
DR

DR N-PSDB; AAQ54652.
XX New chimeric T 84.12 antibody active against carcinoembryonic antigen -
PT has murine variable and human constant regions, also DNA encoding it and
transformed myeloma cells.
XX Claim 1; Page 17; 27pp; English.
XX The sequences (AAQ54651-52) show the light and heavy chain CDNAS of
CC murine T84.12. The T84.12 antibody is directed against the tumour marker
CC carcinoema embryonic antigen, and is useful for tumour imaging and has
CC immunotherapy. The amino acid sequence given in the specification has
CC been incorrectly identified as a nucleic acid sequence, therefore
CC unacceptable characters have been represented as an 'N'. The amino acid
CC sequence given below has been derived from the cDNA, by the indexer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 477 AA;
Alignment Scores:
Pred. No.: 1.29e-101 Length: 477
Score: 1310.50 Matches: 270
Percent Similarity: 68.25% Conservative: 18
Best Local Similarity: 63.98% Mismatches: 39
Query Match: 48.63% Indels: 95
DB: 2 Gaps: 10
US-10-048-116-1 (1-1484) x AAR47450 (1-477)

QY 250 CAAGTGGAGCTGCAAAACATAGCTGCAGAAAACACAACTTGGGAATCTTGACTAAGAGG 309
Db 139 GlnGlyThrLeuAlaThrValSerAlaAlaLys----- 149
QY 310 TCAATTTTCAACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCTCCCAAGTCCCT 369
Db 150 -----ThrThrAlaPro-----SerValTyrProLeuAlaPro 160
QY 370 GTG-----CTGCTGGTGCAGCCCAACACCTTATCTGCTTTTGTGACACACATCTTC 420
Db 161 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 180
QY 421 CCACCTGTGATCAACATCATCATGGTCAAGAAATAGCAATAGCATCATCAGACGCGCTTTAT 480
Db 181 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 197
QY 481 GAGACGAGTCTCTCGTCAACCGTGCACCTTCTTCCCAAGCTGTCTTATCTCACCTTC 540
Db 198 -----HisThrPheProAlaVal----- 203
QY 541 ATCCCTTCTGATGATGATGATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCCG 600
Db 204 -----LeuGlnSerAspLeuTyrThrLeuSer----- 212
QY 601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCTAGAGCTGACAGAAACTGGA 660
Db 213 -----SerSerValThrValThr--- 218
QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAGAGAGCTCCAGGCCCTGGAG 720
Db 219 -----SerSerThr----- 221
QY 721 AAGGAAATGCACAGCTGGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA 780
Db 222 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 234
QY 781 GCATCT-----GAGCCAGAGGGCCCAACAATCAAGCCCTGT 816
Db 235 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 254
QY 817 CCTCCATGCAAAATGCCAGCACCTAACCTTCTTGGTGGAGCCATCCGCTCTTCATCTCCCT 876
Db 255 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 274


```
QY 796 GGGCCCAACATCAAGCCCTGCTCTCCATGCAATGCCAGACCTAACCTCTTGGGTGA 855
Db 100 GlyProThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGlyGly 119
QY 856 CCATCCGCTCTCATCTCCCTCAAGATCAAGATGATGATCATGATCTCCCTGAGCCCC 915
Db 120 ProSerValPheIlePheProLysIleLysAspValLeuMetIleSerLeuSerPro 139
QY 916 ATAGTCACATGCTGCTGGTGGATGGAGGATGCCAGATGCCAGATCTCCAGATCAGCTGG 975
Db 140 IleValThrCysValValAspValSerGluAspProAspValGlnIleSerTrp 159
QY 976 TTTGTGAACAACGCTGAAGCTACACAGCTCAGACACAAACCCATAGAGATTAACAAC 1035
Db 160 PheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsn 179
QY 1036 AGTACTCTCCGGGTGCTAGTCCCTCCATCCAGCAGACAGCTGGATGATGGCAAG 1095
Db 180 SerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLys 199
QY 1096 GAGTTCAATGCAAGGTCAACAAAGACCTCCAGCGCCCATCGAGAGAACCTCTCA 1155
Db 200 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSer 219
QY 1156 AAACCCAAAGGCTCAGTAAGAGCTCCACAGGTATATGCTTGCTCCACAGAGAAGAG 1215
Db 220 LysProLysGlySerValArgAlaProGlnValTyrValLeuProProGluGlu 239
QY 1216 ATGACTAAGAAACAGGTCACTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1275
Db 240 MetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIle 259
QY 1276 TAGCTGGAGTGCACCAACAGCGGAAACAGAGCTAACTACAGAACACTGAACAGTC 1335
Db 260 TyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProVal 279
QY 1336 CTGGACTCTGATGGTTCTTACTTCTATGATGATGATGATGATGATGATGATGATGATGAT 1395
Db 280 LeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrp 299
QY 1396 GTGGAAGAAATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1455
Db 300 ValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisThr 319
QY 1456 ACTNAGGCTTCTCCGGACTCCGGGT 1482
Db 320 ThrLysSerPheSerArgThrProGly 328
```

RESULT 15

AAP93037
ID AAP93037 standard; protein; 447 AA.

AC AAP93037;

DT 25-MAR-2003 (revised)

DT 14-MAR-1990 (first entry)

XX Chimeric antibody heavy chain variable region.

DE KSI/4; chimeric antibody; heavy chain variable region.

KW Mus.

XX BP338767-A..

XX 25-OCT-1989.

XX 18-APR-1989; 89EP-00303814.

XX 21-APR-1988; 88US-00184522.

XX (ELIL) LILLY & CO ELI.

```
XX Beavers LS, Bumol T, Gadsdi RA, Weigel BJ;
PI WPI: 1989-311203/43.
DR N-PSDB; AAN91659.
XX Recombinant DNA cpds. producing antibodies - monoclonal and chimeric
PT derived from monoclonal antibody KSI/4.
XX Claim 6; Page 50; 89pp; English.
XX The sequence encodes the heavy chain of Mab KSI/4, used to construct
CC mouse/human chimeric antibodies. KSI/4 is a murine antibody which binds
CC to surface antigens on adenocarcinoma cells and the use of human C
CC regions avoids immunological problems during treatment. (Updated on 25-
CC MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct FI field.)
XX SQ Sequence 447 AA;
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Alignment Scores:

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Pred. No.: 3 33e-101 Length: 447
Score: 1305.50 Matches: 264
Percent Similarity: 70.65% Conservative: 20
Best Local Similarity: 65.67% Mismatches: 41
Query Match: 48.44% Indels: 77
DB: 1 Gaps: 8
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US-10-048-116-1 (1-1484) x AAP93037 (1-447)

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QY 310 TCAAATTTTCCACCCAGCTACCAATGAGGCTCTCAAGCAGACTGTGTCCCAAGTCCCT 369
Db 111 ThrSerValThrValSerSerAlaLysThrThrAlaProSerValTyrProLeuAlaPro 130
QY 370 GTG-----CTGCTGGTCTGAGCCCAACACCTTATCTGCTTGTGTGACAACTCTTC 420
Db 131 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 150
QY 421 CCACCTGTGATCAACATCACATGATGGCTCAGAAATAGCAAGTCAGTCACACACGCGTTAT 480
Db 151 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerGlyVal--- 167
QY 481 GAGACAGCTTCTCTGCTCAACGCTGACCACTTCTTCCCAAGCTGTCTTATCTCACCTTC 540
Db 168 -----HisThrPheProAlaVal----- 173
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCG 600
Db 174 -----LeuGlnSerAspLeuTyrThrLeuSer----- 182
QY 601 GTTCTGAAACACTGGGACCTGAGATTCAGCCCCCATGTCTAGAGCTGACAGAACTGGA 660
Db 183 -----SerSerValThrValThr----- 188
QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAGAGAGCTCCAGGCGCTGGAG 720
Db 189 -----SerSerThr----- 191
QY 721 AAGGAAATGACACAGCTGGAATGGAGTTGGAAGCACTGGAAGAAAGAACTGCTCAGGCA 780
Db 192 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 204
QY 781 GCATCT-----GAGCCCAAGGGCCCAACATCAAGCCCTGT 816
Db 205 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 224
QY 817 CCTCATGCAATGCCAGCAGCACTTAACCTCTTGGGTGGACCACTCCGCTCTTCTATCTTCCCT 876
Db 225 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 244
QY 877 CCAAGATCAAGATGATGATCTATGATCTCCCTGAGCCCCCATGATGATGATGATGATGAT 936
Db 245 ProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 264
```

Qy	937	GATCTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACGTCGAAGTA	996
Db	265	AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal	284
Qy	997	CACACAGCTCAGACACAAACCATAGAGAGGATTACAACTACTCTCCGGGTGGTCAGT	1056
Db	285	HisThrAlaGlnThrGlnThrHisArgGluAspIyrAsnSerThrLeuArgValValSer	304
Qy	1057	GCCCTCCCCATCCAGCACACAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC	1116
Db	305	AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn	324
Qy	1117	AACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA	1176
Db	325	AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg	344
Qy	1177	GCTCCACAGGTATATGCTTTCCTCCACAGAGAGATGACTAAGAAACAGGTCACCT	1236
Db	345	AlaProGlnValIyrValLeuProProProGluGluMetThrLysLysGlnValThr	364
Qy	1237	CTGACCTGCGATGTCACAGACTTCATCCCTGAAGACATTTACGTGGAGTGGACCAACAAC	1296
Db	365	LeuThrCysMetValThrAspPheMetProGluAspIleIyrValGluTrpThrAsnAsn	384
Qy	1297	GGGAAACAGAGCTAAACTACAGAACACTGAACCACTCCTGGACTCTGATGGTTCTTAC	1356
Db	385	GlyLysThrGluLeuAsnIyrLysAsnThrGluProValLeuAspSerAspGlySerIyr	404
Qy	1357	TTCATGTACAGCAAGCTGAGAGTGGAAAAGAACTGGGTGGAAAGAAATAGCTACTCC	1416
Db	405	PheMetIyrSerIysLeuArgValGluIysLysAsnTrpValGluArgAsnSerIyrSer	424
Qy	1417	TGTTTCAGTGTCCAGGGGTCTGCACAATCACACACGACTAAGAGCTTCTCCCGGACT	1476
Db	425	CysSerValValGlnGluGlyLeuHisAsnHisThrThrLysSerPheSerArgThr	444
Qy	1477	CCGGGT 1482	
Db	445	ProGly 446	

Search completed: June 16, 2005, 02:41:41
Job time : 254.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 16, 2005, 01:36:27 ; Search time 276.5 Seconds
(without alignments)
5496.749 Million cell updates/sec

Title: US-10-048-116-1
Perfect score: 2695
Sequence: 1 atgcgcgtcagcagagctct.....ttctccgcagctccgggtaa 1484

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10048116 @CGN 1.1 307 @runat 15062005 125142 29750 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1313.5	48.7	330	1	GCAA_MOUSE	P01863 mus musculus
2	1313.5	48.7	339	1	GCAM_MOUSE	P01865 mus musculus
3	1297	48.1	472	2	O6PUA7	O6pja7 mus musculus
4	1294.5	48.0	471	2	O66K04	O66k04 mus musculus
5	1291.5	47.9	464	2	O6P295	O6pf95 mus musculus
6	1291.5	47.9	464	2	O6P1P8	O6pjp8 mus musculus
7	1291.5	47.9	465	2	O6P2B2	O6pjb2 mus musculus
8	1182	43.9	256	1	HA2B_MOUSE	P04228 mus musculus
9	1161	43.1	256	2	O6SR48	O6sr48 mus musculus
10	1107	41.1	256	2	O8K2X0	O8k2x0 mus musculus
11	1100	40.8	256	2	O860C1	O860c1 mus musculus
12	1078	40.0	256	1	HA2B_MOUSE	E14434 mus musculus
13	1075	39.9	256	1	HA2K_MOUSE	P01910 mus musculus
14	1058.5	39.3	473	2	O9D8L4	O9d8l4 mus musculus
15	1057	39.2	254	1	HA2J_MOUSE	P23150 mus musculus
16	1048	38.9	254	2	O9TQ71	O9tq71 mus musculus

17	1048	38.9	254	2	O9TQ72	O9tq72 mus musculus
18	1037	38.5	335	1	GCAB_MOUSE	P01864 mus musculus
19	1018.5	37.8	473	2	O91Z05	O91z05 mus musculus
20	1017.5	37.8	474	2	O8R3H6	O8r3h6 mus musculus
21	1012.5	37.6	336	1	GCB_MOUSE	P01866 mus musculus
22	1012.5	37.6	405	1	GBM_MOUSE	P01867 mus musculus
23	1005	37.3	233	1	HA2F_MOUSE	P14435 mus musculus
24	1000	37.1	233	1	HA2R_MOUSE	P14436 mus musculus
25	996	37.0	233	1	HA2S_MOUSE	P14437 mus musculus
26	972	36.1	256	1	HA2B_RAT	P20037 rattus norv
27	964	35.8	256	2	O8V132	O8v132 rattus norv
28	951	35.3	252	2	O70RH9	O70rh9 rattus norv
29	939	34.8	227	1	HA2U_MOUSE	P14438 mus musculus
30	937.5	34.8	255	2	O6MGA0	O6mga0 rattus norv
31	929	34.5	221	1	HA2Q_MOUSE	P04227 mus musculus
32	929	34.5	256	2	O95572	O95572 rattus norv
33	929	34.5	333	1	GCB_RAT	P20761 rattus norv
34	929	34.5	470	2	O7TWK1	O7twk1 mus musculus
35	927.5	34.4	256	2	O8HWL3	O8hw13 sigmodon hi
36	923.5	34.3	329	1	GC3_MOUSE	P22436 mus musculus
37	917.5	34.0	398	1	GC3M_MOUSE	P03987 mus musculus
38	881.5	32.7	458	2	O65ZQ1	O65zq1 homo sapien
39	880.5	32.7	463	2	O99LC4	O99lc4 mus musculus
40	880	32.7	329	1	GCC_RAT	P20762 rattus norv
41	876	32.5	478	2	O6P181	O6p181 homo sapien
42	873.5	32.4	475	2	O6N095	O6n095 homo sapien
43	872	32.4	227	2	O31247	O31247 peromyscus
44	872	32.4	470	2	O6PJA4	O6pja4 homo sapien
45	870	32.3	475	2	O6M2Q6	O6mqz6 homo sapien

ALIGNMENTS

RESULT 1
GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes; further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgeois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a

immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";

RL Eur. J. Biochem. 43:423-435(1974).

RN [5]

RP DISULFIDE BONDS.

RX MEDLINE=7305687; PubMed=4565406;

RA de Preval C., Fougereau M.;

RT "Determination of the primary structure of a mouse gamma G2a

RT immunoglobulin. Identification of the disulfide bridges.";

RL Eur. J. Biochem. 30:452-462(1972).

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; V00798; CAA24178.1; -.

DR PIR; A02152; G2MSA.

DR PDB; 1E4W; X-ray; H=1-99.

DR PDB; 1E4X; X-ray; H/I=1-103.

DR PDB; 1MNU; X-ray; H=1-103.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig.cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS0835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.

FT NON_TER 1 1

FT DOMAIN 6 98 Ig-like 1.

FT DOMAIN 121 220 Ig-like 2.

FT DOMAIN 229 325 Ig-like 3.

FT DISULFID 15 15 Interchain (with a light chain).

FT DISULFID 27 82

FT DISULFID 107 107 Interchain (with a heavy chain).

FT DISULFID 110 110 Interchain (with a heavy chain).

FT DISULFID 112 112 Interchain (with a heavy chain).

FT DISULFID 144 204

FT DISULFID 250 308

FT STRAND 4 4

FT STRAND 7 11

FT STRAND 22 33

FT STRAND 38 41

FT HELIX 42 44

FT TURN 45 45

FT TURN 46 46

FT STRAND 50 52

FT STRAND 56 56

FT TURN 59 60

FT STRAND 62 71

FT TURN 72 77

FT STRAND 81 86

FT HELIX 87 89

FT TURN 90 90

FT STRAND 91 96

SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Alignment Scores:

Pred. No.:

Score: 1.21e-87 Length: 330

Percent Similarity: 71.03% Matches: 267

Best Local Similarity: 67.25% Conservative: 15

Query Match: 48.74% Mismatches: 36

DB: 1 Indels: 79

Gaps: 9

US-10-048-116-1 (1-1484) x GCAA_MOUSE (1-330)

QY 325 GCTACCAATGAGGCTCTCTCAAGCGACTGTGTTCCTCCCAAGTCCCTGTG-----CTG 375

Db 1 AlalysThrThrAlaPro-----SerValTrpLeuAlaProValCysGlyAspThr 18

QY 376 CTGGTCAAGCCCAACACCTTATCTGCTTTGTGTGACAAACATCTTCCACCTGTGATCAAC 435

Db 19 ThrGlySerSerValThrLeuGlyCysLeuValysGlyTyrPheProGluProValThr 38

QY 436 ATCATATGGCTCAGAAATAGCAAGTCTAGTCACAGACGGCGTTTATGAGACAGCTTCTCTC 495

Db 39 LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal----- 50

QY 496 GTCAACCGTGACCATCTCTTCCACAAGCTGCTTATCTCACCTTCTCATCTTCTGTATGAT 555

Db 51 -----HsThrPheProAlaVal-----LeuGlnSer 59

QY 556 GACATTTTATGACTGCAAGGTGGAGCACTGGGGCTTGAGGAGCGGGTCTTGTAAACACTGG 615

Db 60 AspLeuTyrThrLeuSer----- 65

QY 616 GAACCTGAGATTCCAGCCCCCATGTCTAGAGCTGACAGAAACTGGAGTGGAGGATCCACT 675

Db 66 -----SerSerValThrValThr-----SerSer 73

QY 676 ACAGCTCCATCAGCTCAGCTCGAAAGAGCTCCAGGCCCTGGAGAGGAAATGACACAG 735

Db 74 Thr----- 74

QY 736 CTGGAATGGAGTTGCAAGCACTGAAAGAACTGGCTCAGGAGCATCT----- 786

Db 75 -----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLys 92

QY 787 -----GAGCCCAAGAGGGCCCAATCAAGCCCTGTCTCTCATGCAAAATGC 831

Db 93 ValAspLysLysIleGluProArgGlyProThrIleLysProCysProCysLysCys 112

QY 832 CCAGCACTTAACCTCTTTGGGTGGACCATCGTCTTCTATCTTCCCTCCAAAGATCAAGAT 891

Db 113 ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 132

QY 892 GTACTCATGATCTCCCTGAGCCCATAGTCACATGTGTGTGGTGGATGTGAGCGAGAT 951

Db 133 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 152

QY 952 GACCCAGATGTCAGATCAGCTGGTTTGTGAACACGTGAAGTACACAGCTCAGACA 1011

Db 153 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 172

QY 1012 CAAACCCATAGAGAGGATTACAAAGTACTCTCCGGTGGTTCAGTGGCTCCCATCCAG 1071

Db 173 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 192

QY 1072 CACCAGACTGGATGATGGCAAGGAGTTCAAAATGCAAGTCAACAAAGAGCTCCCA 1131

Db 193 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro 212

QY 1132 GCGCCCATCGAGAGACCATCTCAAAACCCAAAGGTTCAGTACAGCTCCACAGGTATAT 1191

Db 213 AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr 232

QY 1192 GTCTTGCTCCACAGAGAGAGATGACTAAGAAACAGGTCTCTGACTGCTGATGGTC 1251

Db 233 ValLeuProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetVal 252

QY 1252 ACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAACACCGGAAACAGAGCTA 1311

Db 253 ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu 272

QY 1312 AACTACAGAGACACTGAAACCACTCCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAG 1371

Db 273 AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys 292

QY 1372 CTGAGAGTGGAAAAGAGAACTGGGTGGAAGAAATAGCTACTCTCTGTTTCTGAGTGGTCCAC 1431


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Db      293 LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis 312
QY      1432 GAGGGTCTGCACAAATCACCACAGACTAAGAGCTTCTCCCGGACTCCGGGT 1482
Db      313 GluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGly 329

RESULT 2
GCAM_MOUSE
ID      GCAM_MOUSE      STANDARD;      PRT;      399 AA.
AC      P01865;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-AUG-1991 (Rel. 19, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Ig gamma-2A chain C region, membrane-bound form.
GN      Name-Ig-1a;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      MEDLINE=8222190; PubMed=6283537;
RA      Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT      "Nucleotide sequences of gene segments encoding membrane domains of
RT      immunoglobulin gamma chains."
RL      Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event-Alternative splicing; Named isoforms=2;
CC      Name=Membrane-bound;
CC      IsoId=P01865-1; Sequence=Displayed;
CC      Name=Secreted;
CC      IsoId=P01864-1; Sequence=External;
CC      Note=Probably the major isoform;
CC      -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@lsb-sib.ch).
CC
CC      EMBL: J00471; AAB59661.1; ALT_INIT.
DR      PIR: A02154; G2MSAM.
DR      PDB: 1K85; X-ray; H=1-100.
DR      PDB: 1K85; X-ray; B=1-101.
DR      PDB: 1YES; X-ray; H=1-99.
DR      MGD: MGI:96443; Ig-1a.
DR      GO: GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR      GO: GO:0003823; F:antigen binding; IDA.
DR      GO: GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR      GO: GO:0006958; P:complement activation, classical pathway; IDA.
DR      GO: GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR      GO: GO:0050728; P:negative regulation of inflammatory response; IDA.
DR      GO: GO:0006910; P:phagocytosis, binding; IDA.
DR      GO: GO:0006911; P:phagocytosis, engulfment; IDA.
DR      GO: GO:0050778; P:positive regulation of immune response; IDA.
DR      GO: GO:0050729; P:positive regulation of inflammatory response; IDA.
DR      GO: GO:0050766; P:positive regulation of phagocytosis; IDA.
DR      GO: GO:0016068; P:Type I hypersensitivity; IDA.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003597; Ig cl.
DR      InterPro: IPR003006; Ig_MHC.
DR      Pfam: PF00047; Ig; 2.
DR      SMART: SM00407; IG1; 2.
DR      PROSITE: PS50835; IG LIKE; 3.
DR      PROSITE: PS00290; IG MHC; 1.
KW      3D-structure; Alternative splicing; Glycoprotein;
KW      Immunoglobulin C region; Immunoglobulin domain; Repeat; Transmembrane.
FT      NON_TER      1
FT      DOMAIN      6 98      Ig-like 1.
FT      DOMAIN      121 220      Ig-like 2.

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FT      DOMAIN      229      325      Ig-like 3.
FT      DISULFID      15      Interchain (with a light chain).
FT      DISULFID      27      82
FT      DISULFID      107      107      Interchain (with a heavy chain).
FT      DISULFID      110      110      Interchain (with a heavy chain).
FT      DISULFID      112      112      Interchain (with a heavy chain).
FT      DISULFID      144      204
FT      DISULFID      250      308
FT      TRANSMEM      346      363      Potential.
FT      DOMAIN      364      399      Cytoplasmic (Potential).
FT      CARBOHYD      180      180      N-linked (GlcNAc...) (Potential).
FT      STRAND      7      11
FT      STRAND      22      33
FT      STRAND      38      41
FT      HELIX      42      44
FT      TURN      45      45
FT      STRAND      46      46
FT      TURN      48      49
FT      STRAND      50      58
FT      TURN      59      60
FT      STRAND      61      71
FT      TURN      72      77
FT      STRAND      81      86
FT      HELIX      87      89
FT      TURN      90      90
FT      STRAND      91      96
SQ      SEQUENCE      399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Alignment Scores:
Pred. No.:      1.26e-87      Length:      399
Score:      1313.50      Matches:      267
Percent Similarity:      71.03%      Conservative:      15
Best Local Similarity:      67.25%      Mismatches:      36
Query Match:      48.74%      Indels:      79
DB:      1      Gaps:      9

US-10-048-116-1 (1-1484) x GCAM_MOUSE (1-399)
QY      325 GCTACCAATGAGGCTCCTCAAGCGACTGTTCCCAAGTCCCTGTG-----CTG 375
Db      1 AlaLysThrAlaPro-----SerValTyProLeuAlaProValCysGlyAspThr 18
QY      376 CTGGGTGAGCCCAACACACCTTATCTGCTTGTGGACAACATCTCCACCTGTGATCAAC 435
Db      19 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyPheProGluProValThr 38
QY      436 ATCAGATGGCTCAGAAATAGCAAGTCAAGTCAGACAGCGCGTGTATGAGACCGATTCCTC 495
Db      39 LeuThrTriP-----AsnSerGlySerLeuSerSerGlyVal-----50
QY      496 GTCACACCGTGACCATCTCCACAGCTGTCTATCTCACCTTCATCCTCTCTGTGATGAT 555
Db      51 -----HisThrPheProAlaVal-----LeuGlnSer 59
QY      556 GACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGCGTTCCTGAAACACTGG 615
Db      60 AspLeuTyThrLeuSer-----65
QY      616 GAACCTGAGATTCCAGCCCCCATGTGACAGCTGACAGAAACTGGAGGTGGAGGATCCACT 675
Db      66 -----SerSerValThrValThr-----SerSer 73
QY      676 ACAGTCCATCAGCTCAGTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAATGACAG 735
Db      74 Thr-----74
QY      736 CTGGAATGGAGTGTCAAGCACTGGAAGAAAGAACTGGCTCAGGACGACATCT-----786
Db      75 -----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLys 92
QY      787 -----GAGCCCGAGAGGGCCCAACATCAAGCCCTGTCTCCATGCAATGC 831

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Db 93 ValAspLysLysIleGluProArgGlyProThrIleLysProCysProProCysLysCys 112
 Qy 832 CCAGCACCTAACCTCTTGGTGGACCATCCGTCCTTCATCTTCCTCCCAAGATCAAGAT 891
 Db 113 ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 132
 Qy 892 GTACTCATGATCTCCCTGAGCCCATAGTCACATGTCGTGGTGGTGGATGTCAGCGAGAT 951
 Db 133 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 152
 Qy 952 GACCAGATGTCAGATCAGCTGGTGTGTGTAACACGTCGGAAGTACACACAGCTCAGACA 1011
 Db 153 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 172
 Qy 1012 CAACCCCATAGAGGATTACAACAGTACTCTCCGGTGGTGCAGTGCCTCCCATCCAG 1071
 Db 173 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 192
 Qy 1072 CACGAGGACTCGATGAGTGGCAAGGATTCAAATGCAAGGTCAACACAAAGACTCCCA 1131
 Db 193 HisGlnAspTrpMetSerGlyLeuGluPheLysCysLysValAsnAsnLysAspLeuPro 212
 Qy 1132 CGCGCCATCGAGAAACCATCTCAAAACCCAAAGGTCAGTAAGAGTCCACAGGTATAT 1191
 Db 213 AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr 232
 Qy 1192 GTCTTGCTCCACAGAAAGAGATGACTAAGAAACAGGTCACTCTGACTGATCGATGGTC 1251
 Db 233 ValLeuProProProGluGluMetThrLysLysGlnValThrLeuThrCysMetVal 252
 Qy 1252 ACAGACTTCATGCTGAGACATTTACGTGAGTGGACCAACCAACGCGGAAACAGAGCTA 1311
 Db 253 ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu 272
 Qy 1312 AACTACAGAACACTGAACCACTGCTGAGTCTCTGATGGTCTTACTTCTCATGTACAGCAAG 1371
 Db 273 AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys 292
 Qy 1372 CTGAGAGTGGAAAGAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTTCAAGTGGTCCAC 1431
 Db 293 LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis 312
 Qy 1432 GAGGCTCGCACATCACACACGACTAAGAGCTTCTCCCGAGCTCCGGGT 1482
 Db 313 GluGlyLeuHisAsnHisThrThrLysSerPheSerArgThrProGly 329
 RESULT 3
 Q6PUA7
 ID Q6PUA7 PRELIMINARY; PRT; 472 AA.
 AC Q6PUA7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018535; AAH18535.1; -.
 DR HSSP; P01865; 1KB5.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGcl; 3.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;
 Alignment Scores:
 Pred. No.: 2,11e-86 Length: 472
 Score: 1297.00 Matches: 273
 Percent Similarity: 64.47% Conservative: 30
 Best Local Similarity: 58.09% Mismatches: 85
 Query Match: 48.13% Indels: 82
 DB: 11 Gaps: 11
 US-10-048-116-1 (1-1484) x Q6PUA7 (1-472)
 Qy 115 GTTATCAGTCTCTCGGAGACATTTGCCAGTACACATCAATTTGATGATGAGTTG 174
 Db 70 IleTyrProAsnAsnGlyGlyAsnGly---TyrAsnGlnLysPheLysGlyLysAlaThr 88
 Qy 175 TTCTATCTGGACTGGGATAGAAGAAACTGTCTGGAGGCTTCTCTGAGTTT----- 225
 Db 89 LeuThrValAspLysSerSerSerThrAlaTyrMetGluLeuArgSerLeuThrSerGlu 108
 Qy 226 GGCCAAATTGATCTCTTTGAGCCCCCAAGTGGAGTGCAGAAACATAGCTGCAGAAAAACAC 285
 Db 109 AspSerAlaValTyrTyrCysAlaArgGlyTyrIleSerTyrTyrSerTyrAsp---His 127
 Qy 286 AACTTGGGAATCTTGAATAAGAGGTCAAATTTCAACCCAGCTACCAATGAGGCTCTCCAA 345
 Db 128 TyrPheAspTyrTrpGlyGlnGlyThrThrIleThrValSerSerAlaLysThrAla 147
 Qy 346 CGGACTGTGTCCCAAGTCCCTGTG-----CTGTGGGTGACCCCAACACACCTT 396
 Db 148 ProSerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSerValThrLeu 167
 Qy 397 ATCTGCTTTGTGGACAACATCTTCCACCTGTGATCAACATCAATCGTCAGAAATAGC 456
 Db 168 GlyCysLeuValLysGlyTyrPheProGluProValThrLeuThrTrp-----AsnSer 185
 Qy 457 AAGTCAGTCACAGCGGCTTTATGAGACCAGCTTCTCTCGTCAACCGGTGACCATTCCTTC 516
 Db 186 GlySerLeuSerSerGlyVal-----HisThrPhe 195
 Qy 517 CACAGCTGTCTTATCTCATCTTCATCTCTGATGATGACATTTATGATGCTGAAGGTG 576
 Db 196 ProAlaVal-----LeuGlnSerAspLeuTyrThrLeuSer--- 207
 Qy 577 GAGCACTGGGCGCTGGAGGAGCGGTTCTGAAACACATGGGAACCTGAGATTCACAGCCCCC 636

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Db 207 ----- 207
QY 637 ATGTCAGAGCTGACAGAACTGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTC 696
Db 208 ---SerSerValThrValThr-----SerSerThr----- 216
QY 697 GAAAAAGAGCTCCAGGCCCTGGGAGAGGAAATATGCACAGCTGGAATGGAGTTGCAAGCA 756
Db 217 ----- 221
QY 757 CTGGAAGAGAACTGGCTCAGGCAGAGCTCT-----GAGCCC 792
Db 222 IleThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGluPro 241
QY 793 AGAGGGCCCAATCAAGCCCTGCTCCATGCAATGCCAGCAGCCCACTCACTCTGGGT 852
Db 242 ArgGlyProThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGly 261
QY 853 GGACCATCCGTCCTTCTATCTTCCCTCAAGATCAAGATGATCATGATCTCCCTGAGC 912
Db 262 GlyProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSer 281
QY 913 CCATAGTCACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
Db 282 ProMetValThrCysValValValValValValValValValValValValValValVal 301
QY 973 TGGTTTGTGAACACCTGGAAGTACACACAGCTCAGACACACACACACACACACACACAC 1032
Db 302 TrpPheValAsnAsnValGluValLeuThrAlaGlnThrGlnThrHisArgGluAspTyr 321
QY 1033 AACAGTACTCTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1092
Db 322 AsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGly 341
QY 1093 AAGGAGTTCAATGCAAGGTCAACACAAAGACTCTCCAGCGGCCCATCGAGAGAACATC 1152
Db 342 LysGluPheLysCysLysValAsnAsnLysAlaLeuProAlaProIleGluArgThrIle 361
QY 1153 TCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTGCTCCACCAAGAGAA 1212
Db 362 SerLysProLysGlySerValArgAlaProGlnValThrValLeuProProGluGlu 381
QY 1213 GAGATGACTAAGAAACAGGTCTACTGACCTGTCATGCTGATGCTCAGACATTCATGCTGAAGAC 1272
Db 382 GluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAsp 401
QY 1273 ATTTAGCTGGAGTGGACCAACAAACGGGAAACAGAGCTAACTACAGAACACTGAACCA 1332
Db 402 IleTyrValGluThrThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluPro 421
QY 1333 GTCCTGGACTCTGATGTTCTTACTTCATGTCAGCAAGCTGAGCTGGAAAGAGAGAAC 1392
Db 422 ValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsn 441
QY 1393 TGGGTGGAAGAAATAGCTACTCTGTTTCAGTGGTCCACGAGGTCTGCACAAATCACCAC 1452
Db 442 TrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHis 461
QY 1453 ACAGCTAAGAGCTTCTCCCGACTCCGGGT 1482
Db 462 ThrThrLysSerPheSerArgThrProGly 471
RESULT 4
Q66K04
ID Q66K04 PRELIMINARY; PRT; 471 AA.
AC Q66K04;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080671; AAH80671.1; --
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 52258 MW; 81BB7C322B315AC2 CRC64;
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Alignment Scores:

Pred. No.:	3,22e-86	Length:	471
Score:	1294.50	Matches:	271
Percent Similarity:	65.50%	Conservative:	29
Best Local Similarity:	59.17%	Mismatches:	59
Query Match:	48.03%	Indels:	99
DB:	2	Gaps:	11

US-10-048-116-1 (1-1484) x Q66K04 (1-471)

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QY 160 GATGGTGTAGTGTGTCTTCTATGTGGACTTGGATAGAGAAACT-----GTC 207
Db 95 AspSerGlnSerMetLeuTyrLeuGlnMetAsnLeuLysThrGluAspThrAlaMet 114
QY 208 TGGAGGCTCTCTGAGTTTGGCCAATTG-----ATACTCTTTGAGCCCAAGGTGGACTG 261
Db 115 TyrTyrCysValLysGluGlyGlnLeuGlyProTyrTyrPheAspTyrTrpGly----- 132
QY 262 CAAAAATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGAGGTCAAAATTCACC 331
Db 133 -----GlnGlyThrThrIleThr 138
QY 322 CCAGCTACCAATGAGGCTCTCAAGCGACTGTGTCCCAAGTCCCTCTG----- 372
Db 139 ValSerSerAlaLysThrThrAlaProSerValTyrProLeuAlaProValCysGlyAsp 158
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Qy	167	----	ATGACTTGT	----	175
Db	26	SerGlyAlaGluLeuValArgProGlyAlaSerValLysLeuSerCysLysAlaSerGly	45		
Qy	176	-----TCTATGTGGACT-----	TGGTAAGAAGAAACACTGCTCGGAGGCTT-----	216	
Db	46	TyrIlePheThrSerTyrTrpIleHisTyrTrpValLysGlnArgSerGlyGlnGlyLeuGlu	65		
Qy	217	-----CCTGAGTTTGGCCAAATTGATACTCTTTGAGCCCCCAAGGTGGA	258		
Db	66	TrpIleAlaArgIleTyrProGlyThrGlySerThrTyrTyrAsnGluLysPheLysGly	85		
Qy	259	CTGCAAAACATAGCTGCAGAAAAACACAACTCTGGGAATCTTGACTAAGAGGTCAAATTC	318		
Db	86	LysAlaThrLeuThrAlaAspLysSerSerThrAlaPheMetGlnLeuSerSerLeu	105		
Qy	318	-----	-----	318	
Db	106	LysSerGluAspSerAlaValTyrPheCysAlaTyrGlyTyrAspAlaLeuTyrTrpGly	125		
Qy	319	-----ACCCAGCTACCAATGAGGCTCCTCAAGCGACT-----	TGTTTCCCCCAAG	363	
Db	126	GlnGlyThrProIleThrValSerSerAlaLysThrThrAlaProSerValTyrProLeu	145		
Qy	364	TCCCTGTG-----CTGCTGGGTGAGCCCAACACCCCTTATCTCTTTGTGGACAAC	414		
Db	146	AlaProValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGly	165		
Qy	415	ATCTTCCCACTGTGATCAACATCACATGCTGCAAAATAGCAAGTCAGTCACAGAGCGC	474		
Db	166	TyrPheProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGly	183		
Qy	475	GTTTATGAGACCAAGCTTCTCTGTCACCGTGACCAATTCCTTCCACAAGCTGTCTTATCTC	534		
Db	184	Val-----HisThrPhePro-----	188		
Qy	535	ACCTTCATCCCTTCTGATGATGACATTATGACTGCAAGGTGGAGCACTGGGGCTGGAG	594		
Db	189	-----ValValLeuGlnSerAspLeuTyrThrLeuSer-----	199		
Qy	595	GAGCGGTTCTGAACAACACTGGAAACCTGAGATTCACGCCCCATGTTCAGAGCTGACAGAA	654		
Db	200	-----SerSerValThrVal-----	204		
Qy	655	ACTGGAGGTGGAGGATCCATACAGCTCCATCAGCTCAGCTCGAANAAGAGCTCCAGGCC	714		
Db	205	Thr-----SerSerThr-----	208		
Qy	715	CTGAGAAGGAAAAATGCACAGCTGGAAATGGGAGTTGCAAGCACCTGGAAGAAAGGAACCTGGCT	774		
Db	209	-----TrpProSerGlnSerIleThrCysAsnValAla-----	219		
Qy	775	CAGCAGCATCT-----GAGCCAGAGGGCCCCACAATCAAG	810		
Db	220	HisProAlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLys	239		
Qy	811	CCCTGTCTCCATCCAAATCCCGAGCACTTAACCTCTTGGGTGGACCATCCGCTTTCATC	870		
Db	240	ProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIle	259		
Qy	871	TTCCCTCCAAGATCAAGGATGTACTCATGTCTCTCCCTGAGCCCCATAGTCACATGTGTG	930		
Db	260	PheProProLysIleLysAspValLeuMetIleSerLeuSerProMetValThrCysVal	279		
Qy	931	GTGGTGGATGTGACGGAGGATGACCCAGATGTCCAGATCAGCTGGTTGTGCAACAACGTG	990		
Db	280	ValValAspValSerGluAspProAspValGlnIleSerTrpPheValAsnAsnVal	299		
Qy	991	GAGTACACAGCTCAGACACAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTG	1050		
Db	300	GluValLeuThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVal	319		

QY	1051	GTCAGTCCCTCCCATTCCACGACCAGGACTGGATGAGTGCGCAAGGAGTTCAAATGCAAG	1111
Db	320	ValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLeysGluPhelYeCysLys	339
QY	1111	GTCACAACAAGAAGCTCCCGAGCGCCCATCGAGAGAACCATCTCAAAACCCAAGGGTCA	1170
Db	340	ValAsnAnlNylsalaleuProAlaprolleGlUargThrileserlySProLySGlySer	359
QY	1171	GTAAGAGCTCCACAGGTATATGTCTTGCTCCACGAGAAGAGATGACTAAGAAAACAG	1230
Db	360	ValArgalaProGlnValTyValleuProProProGluGluMetThrLysLysGln	379
QY	1231	GTCAGTCTGCATCGTGTACAGACTTCATGCTCGGAACACATTTACGTGGAGTGGACC	1290
Db	380	ValThrLeuthrCySmetValThrAspPheMetProGluaspileytyrValGluIrrpThr	399
QY	1291	AACAACGGGAAAAACAGAGCTATAACTACAAGAACACTGAAACACAGTCCCTGGAGCTCTGATGGT	1350
Db	400	AsnAnnglyysThrGluLeuasntyFlyeAsnThrCluProValleuaspSeraspGly	419
QY	1351	TCTTACTTTCATGACAGCAAGCTCGAGAGTGGAAAAGAAAGAACTGGGTGGAAAAGAAATAGC	1410
Db	420	SerTyPheMetTySerLysLeuArgValglulyslysAsnTrpValGluArGAsnSer	439
QY	1411	TACTCTGTTTCAGTGTCCACGAGGCTGTGCACAAATCACACAGGACTAAGAGCTTCTCC	1470
Db	440	TyrSerCySerValValHisGluGlyLeuHieAsnHisHishThrThrLysSerLeuSer	459
QY	1471	CGGACTCGGGGT 1482	
Db	460	ArgThrProGly 463	
RESULT	6		
Q6PIP8		PRELIMINARY;	PRT; 464 AA.
ID	Q6PIP8		
AC	Q6PIP8;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_Taxid	10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II; TISSUE=Mammary tumor;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.-I., Wang J., Haieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,		
RA	Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,		
RA	Raba S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II; TISSUE=Mammary tumor;		
RA	Strauberg R.;		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		

Qy	997	CACACAGCTCAGACACAAAACCCATAGAGAGGATTACAAACAGTACTCTCCCGGTTGGTCAGT	1056
Db	302	LeuThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer	321
Qy	1057	GCCTCTCCCATCCAGACACACAGGACTGATGAGTGGCAGAGGTTCAAATGCAAGGTCAAC	1116
Db	322	AlaLeuProIleGlnHisGlnAspTyrMetSerGlyLysGluPheLysCysLysValAsn	341
Qy	1117	AACAAAGACCTCCAGCGCCCATCGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA	1176
Db	342	AsnLysAlaLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg	361
Qy	1177	GCTCCACAGGTATATGCTTTCGCTCCACACAGAGAAGAGATGACTAAGAAACAGGTCACT	1236
Db	362	AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr	381
Qy	1237	CTGACCTGCATGFTCAAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAAC	1296
Db	382	LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTyrThrAsnAsn	401
Qy	1297	GGGAAACAGAGCTAAACTACAAACACACTGAACCACTCTCGACTCTGTGATGGTCTCTAC	1356
Db	402	GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr	421
Qy	1357	TTCATGTACAGCAAGCTGACAGTGGAAAGAAAGAACTCGGCTGGAAGAAATAGTACTCC	1416
Db	422	PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer	441
Qy	1417	TGTTCAAGTGTCTCCAGAGGCTCTGCACAAATCACACACAGACTAAGAGCTTCTCCCGACT	1476
Db	442	CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThr	461
Qy	1477	CCGGGT 1482	
Db	462	ProGly 463	
RESULT 7			
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ID	Q6PJB2	PRELIMINARY;	PRT; 465 AA.
AC	Q6PJB2;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxId	10090;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II; TISSUE=Mammary tumor;		
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		

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[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;

Alignment Scores:
Pred. No.: 5,33e-86 Length: 465
Score: 1291.50 Matches: 262
Percent Similarity: 70.15% Conservative: 20
Best Local Similarity: 65.17% Mismatches: 43
Query Match: 47.92% Indels: 77
DB: 2 Gaps: 8

US-10-048-116-1 (1-1484) x Q6FJB2 (1-465)
QY 310 TCAATTTTCAACCCAGCTACCAATGAGGCTCTCAAGCAGCTGTGTTCCCAAGTCCCT 369
DB 129 ThrThrIleThrValSerSerAlaLysThrThrAlaProSerValThrProLeuAlaPro 148
QY 370 GTG-----CTGCTGGTACGCCCAACACCCCTTATCTGCTTTGTGGACAAACATCTTC 420
DB 149 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 168
QY 421 CCACCTGTGATCAATCATCATCGCTCAGCAATAGCAATGCAAGTCAGTCACAGCGGCTTAT 480
DB 169 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 185
QY 481 GAGACACGCTTCTCGTCAACCGTGACCATTCCTCCACAAGCTGTCTTATCTCACCTTC 540
DB 186 -----HisThrPheProAlaVal----- 191
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCAGCTGGGGCTGGAGAGCCG 600
DB 192 -----LeuGlnSerAspLeuTyrThrLeuSer----- 200
QY 601 GTTCTGAACACTGGGNACTGAGATTCAGACCCCATGTCAGAGCTGACAGAAACTGGA 660
DB 201 -----SerSerThr-----SerSerValThrValThr--- 206
QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAGAGAGCTCCAGGCGCTGGAG 720
DB 207 -----SerSerThr----- 209
QY 721 AAGGAAATGTCACAGCTGGGATCGGATGCGAGTTGCAAGCACTGGAAAGAACTGGCTCAGGCA 780
DB 210 -----TyrProSerGlnSerIleThrCysAsnValAlaHisPro 222
QY 781 GCATCT-----GAGCCAGAGGGCCCAATCAATCAAGCCCTGT 816
DB 223 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 242
QY 817 CTCCCAATGAAATGCCAGACCTAACTCTCGGTGGACCATCCGCTTCTCATCTTCCCT 876
DB 243 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 262
QY 877 CCAAGATCAAGGATGTACTCATGTATCCCTGAGGCCCATAGTCATGTGTGGTGGTG 936
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Db 263 ProLysIleLysAspValLeuMetIleSerLeuSerProMetValThrCysValValVal 282
QY 937 GATGTGAGCGAGGATGATCACCAGATGTCACAGATCAGCTGTTTGTGAACACGTTGGAGTA 996
Db 283 AspValSerGluAspAspProaspValGlnIleSerIrrPheValAsnAsnValGluVal 302
QY 997 CACACAGCTCAGACACAAACCCATAGAGAGGATTACACAGTACTCTCCGGGTGGTCAGT 1056
Db 303 LeuThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer 322
QY 1057 GCCTCCCATCCAGCACCAGGACTGGATGAGTGGCAAGAGTTCAATGCAAGGTCACAC 1116
Db 323 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 342
QY 1117 AACAAAGACCTCCCGCGCCCATCGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA 1176
Db 343 AsnLysAlaLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 362
QY 1177 GTCCACAGGTATGTCTTGTCTCCACAGAGAGAGATGACTAAGAAACAGGTCACCT 1236
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QY 1237 CTGACCTGATGCTCAGACACTTCATGCTGCTGAAGACATTTACGTGAGTGGACCAACAC 1296
Db 383 LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn 402
QY 1297 GGGAAACAGAGCTAAACTACAAGACACTGGAACAGTCTGGACTCTGATGTTCTTAC 1356
Db 403 GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr 422
QY 1357 TTCTGTGTCAGCAAGCTGAGAGTGGAAAGAGAACTGGGTGGAAAGAAATAGCTACTCC 1416
Db 423 PheMetTyrSerLysLeuArgValGluLysLysAsnTyrValGluArgAsnSerTyrSer 442
QY 1417 TGTTCAGTGGTCCACAGGCTCTGCAATCACCACACAGCTAAGAGCTTCTCCCGGACT 1476
Db 443 CysSerValValHisGluGlyLeuHisAsnHisThrThrLysSerPheSerArgThr 462
QY 1477 CCGGGT 1482
Db 463 ProGly 464

RESULT 8
HA2D MOUSE STANDARD; PRT; 256 AA.
ID HA2D MOUSE
AC P04228;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE H-2 class II histocompatibility antigen, A-D alpha chain precursor.
GN Name=H2-Aa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83285339; PubMed=6309407; DOI=10.1016/0092-8674(83)90147-2;
RA Benoist C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;
RT "Regions of allelic hypervariability in the murine A alpha immune
response gene."
RL Cell 34:169-177(1983).
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CC or send an email to license@isb-sib.ch).
DR EMBL; K01923; AAA39615.1; -.
DR PIR; A02219; HLMSA2.
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DR PDB: 1ES0; X-ray; A=24-213
DR PDB: 1F3J; X-ray; A/D=27-208.
DR MGD; MGI:95895; H2-Aa.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00993; MHC_II_alpha; 1.
DR SMART; SM00407; IGG1; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0290; IG MHC; 1.
KW 3D-structure; Glycoprotein; MHC II; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 256 H-2 class II histocompatibility antigen,
FT DOMAIN 24 111 A-D alpha chain.
FT DOMAIN 112 205 Extracellular alpha-1.
FT DOMAIN 206 218 Extracellular alpha-2.
FT TRANSMEM 219 244 Connecting peptide.
FT DOMAIN 245 256 Cytoplasmic tail.
FT DISULFID 134 190 By similarity.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT STRAND 31 42
FT TURN 43 45
FT STRAND 46 53
FT TURN 54 55
FT STRAND 56 62
FT TURN 63 66
FT STRAND 67 70
FT TURN 73 74
FT TURN 83 83
FT HELIX 84 103
FT TURN 104 105
FT STRAND 115 120
FT TURN 126 127
FT STRAND 130 139
FT STRAND 145 150
FT TURN 151 152
FT STRAND 153 155
FT STRAND 159 161
FT STRAND 165 166
FT TURN 168 169
FT STRAND 172 180
FT STRAND 188 193
FT TURN 195 196
FT STRAND 201 205
SQ SEQUENCE 256 AA; 28243 MW; 085B3FE643B58BBB CRC64;

Alignment Scores:
Pred. No.: 4.92e-78 Length: 256
Score: 1182.00 Matches: 219
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.86% Indels: 0
DB: 1 Gaps: 0

US-10-048-116-1 (1-1484) x HA2D_MOUSE (1-256)

QY 1 ATGCGGTGCAGCAGCTCTGATTCGGGGTCTCGCCCTGAACACCATGCTCAGCCTC 60
DB 1 MetProCy8SerArgAlaLeuIleGlyValleuAlaLeuAnThrMetLeuSerLeu 20
QY 61 TGGCGAGGTGAAGACGACATTGAGCGCCGACACGCTAGCTTCTATGTGTACAACTGTTTAT 120
DB 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40
QY 121 CAGTCTCTGAGACATTGGCCATACACATCAATTTGATGCTGATGAGTTGTTTCTAT 180
DB 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
QY 181 GTGGACTTGGATAAGAAAGAACTGTCTGGAGGCTCTCTGAGTGTGGCAATTGATCTC 240

Db 61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80
QY 241 TTTGAGCCCAAGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATTTG 300
Db 81 PheGluProGlnGlyLeuGlnAsnIleAlaAalaGluLysHisAsnLeuGlyIleLeu 100
QY 301 ACTAAGAGGTCAAATTTTCAACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCCC 360
Db 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
QY 361 AAGTCCCTCTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420
Db 121 LysSerProValleuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
QY 421 CCACCTGTGATCAACATCATCGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
QY 481 GAGACGAGCTTCTCTCGTCAACCGTGACCATCTTCCACAGCTGTCTTATCTCACCTTC 540
Db 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
QY 541 ATCCCTTCTGATGATGATCATTTATGACTGCAAGGTGAGCACTGGGGCTGGAGAGCCG 600
Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
QY 601 GTTCTGAACACTGGGAACCTGAGATTCAGATTCAGCCCCCATGTTCAGAGCTGCAGAGAACT 657
Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219

RESULT 9
Q6SR48 PRELIMINARY; PRT; 256 AA.
ID AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE H-2 class II histocompatibility antigen, A-D alpha chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Gao M., Wang H., Wang Q.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY452201; AAR19089.1; -.
DR HSSP; P14438; IK2D
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; F: MHC class II receptor activity; IEA.
DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . . ; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00993; MHC II alpha; 1.
DR SMART; SM00407; IGG1; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 256 AA; 28178 MW; A7EE3448FE5CAA88 CRC64;

Alignment Scores:
Pred. No.: 1.7e-76 Length: 256
Score: 1161.00 Matches: 216
Percent Similarity: 99.09% Conservative: 1
Best Local Similarity: 98.63% Mismatches: 2
Query Match: 43.08% Indels: 0
DB: 2 Gaps: 0


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US-10-048-116-1 (1-1484) x Q6SR48 (1-256)
QY 1 ATGCGGTGACGAGAGCTGTGATTTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTC 60
DB 1 MetProCysSerArgAlaLeuLeuLeuGlyValLeuAlaLeuAnThrMetLeuSerLeu 20
QY 61 TCGGAGGTGAAGACGACATTTAGGCGCCAGCAGTGGCTTCTATGGTACAACTGTTTAT 120
DB 21 CysGlyGlyGluAspValIleGluAlaAspHisValGlyPheTyrGlyThrValTyr 40
QY 121 CAGTCTCTGAGACATTTGGCCAGTACACATGAATTTGATGGTGTGATGTTTCTAT 180
DB 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
QY 181 GTGGACTTGTGATAAGAAAGAACTGCTGGAGGCTTCTCAGTGTGGCCAAATGATCTC 240
DB 61 ValAspLeuAspIleGlyThrValTyrPargLeuProGluPheGlyGlnLeuLeuLeu 80
QY 241 TTGAGCCCCAAGGTGAGCTGCAAAACATAGCTGCAGAAACACAACTTTGGGAATCTTG 300
DB 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaGluLysHisAsnLeuGlyIleLeu 100
QY 301 ACTAAGAGTCAATTTCCACCCAGCTACCAATGAGCTCTCAAGGACTGTGTTCCCTC 360
DB 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
QY 361 AAGTCCCTCTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGACACATCTTC 420
DB 121 LysSerProValLeuLeuGlyGlnProHisThrLeuIleCysPheValAspAsnIlePhe 140
QY 421 CCACCTGTGTATCAACATCATCATGGCTCAGAAATAGCAAGTCAGTCACAGCGCGTTTAT 480
DB 141 ProProValIleAsnIleThrTyrLeuArgAsnSerLysSerValThrAspGlyValTyr 160
QY 481 GAGACAGCTTCTCTGTCACCGTACCATCTCTTCCACAGCTGTCTTATCTCAGCTTC 540
DB 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
QY 541 ATCCCTTCTCATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGGACCG 600
DB 181 IleProSerAspAspIleTyrAspCysLysValGluHisTyrGlyLeuGluGluPro 200
QY 601 GTTCTGAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGTGACAGAAACT 657
DB 201 ValIleLysHisTyrGluProGluIleProAlaProMetSerGlyLeuThrGluThr 219
RESULT 10
ID Q8K2X0 PRELIMINARY; PRT; 256 AA.
AC Q8K2X0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE H2-Aa protein.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029620; AAH29620.1; -.
DR HSSP; P14438; IK2D.
DR MGD; MGI:95895; H2-Aa.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005764; C:lysosome; IDA.
DR GO; GO:0042613; C:MHC class II protein complex; IDA.
DR GO; GO:0045012; F:MHC class II receptor activity; IDA.
DR GO; GO:0042605; F:peptide antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042591; P:antigen presentation, exogenous antigen via. . ; IDA.
DR GO; GO:0048005; P:antigen presentation, exogenous peptide ant. . ; IDA.
DR GO; GO:0045582; P:positive regulation of T-cell differentiation; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001003; MHC II_alpha.
DR Pfam; PF07654; C1-set; 1_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 256 AA; 28158 MW; DDBBAA26D74219E CRC64;
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Alignment Scores:

Pred. No.:	1,54e-72	Length:	256
Score:	1107.00	Matches:	205
Percent Similarity:	94.98%	Conservative:	3
Best Local Similarity:	93.61%	Mismatches:	11
Query Match:	41.08%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116-1 (1-1484) x Q8K2X0 (1-256)

QY	1	ATGCCGTGACGAGAGCTGTGATTTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTC	60
DB	1	MetProCysSerArgAlaLeuLeuLeuGlyValLeuAlaLeuAnThrMetLeuSerLeu	20
QY	61	TCGGAGGTGAAGACGACATTTAGGCGCCAGCAGTGGCTTCTATGGTACAACTGTTTAT	120
DB	21	CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyIleValTyr	40
QY	121	CAGTCTCTGAGACATTTGGCCAGTACACATGAATTTGATGGTGTGATGTTTCTAT	180
DB	41	GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyrPheTyr	60
QY	181	GTGGACTTGGATAAGAAAGAAACTGCTGGAGGCTTCTCGAGTTTGGCCAAATGATCTC	240
DB	61	ValAspLeuAspIleGlyThrValTyrMetLeuProGluPheGlyGlnLeuThrSer	80
QY	241	TTTGAGCCCCAAGGTGAGCTGCAAAACATAGCTGCAGAAACACAACTTTGGGAATCTTG	300
DB	81	PheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGlyTyr	100
QY	301	ACTAAGAGTCAATTTCCACCCAGCTACCAATGAGCTCTCCTCAAGGACTGTGTTCCCTC	360
DB	101	ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro	120

[1] SEQUENCE FROM N.A.
 RA Rowen L., Qin S., Ahearn M.E., Loretz C., Faust J., Lasky S.,
 RA Mahairas G., Hood L.E.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Rowen L., Qin S., Loretz C., Mix L., Lasky S., Madan A., Hood L.E.;
 RA "Sequence of the mouse major histocompatibility class II region";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN SEQUENCE OF 9-256 FROM N.A.
 RX MEDLINE=83285339; PubMed=6309407; DOI=10.1016/0092-8674(83)90147-2;
 RA Benoist C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;
 RA "Regions of allelic hypervariability in the murine A alpha immune
 RT response gene";
 RL Cell 34:169-177(1983).
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 CC -----
 DR EMBL; AF027865; AAB81529.1; -
 DR EMBL; AF050157; AAC05285.1; -
 DR EMBL; BC019721; AAH19721.1; -
 DR EMBL; BC031711; AAH31711.1; -
 DR EMBL; K01922; AAA39614.1; -
 DR PDB; 1LNU; X-ray; A/C/E/G=27-208.
 DR PDB; 1MUJ; X-ray; A=24-219.
 DR MGD; MGI:95895; H2-Aa.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001003; MHC_II_alpha.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00993; MHC_II_alpha; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW 3D-structure; Glycoprotein; MHC II; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 256 H-2 class II histocompatibility antigen,
 FT A-B alpha chain.
 FT DOMAIN 24 111 Extracellular alpha-1.
 FT DOMAIN 112 205 Extracellular alpha-2.
 FT DOMAIN 206 218 Connecting peptide.
 FT TRANSMEM 219 244

FT DOMAIN 245 256 Cytoplasmic tail.
 FT DISULFID 134 190 By similarity.
 FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 256 AA; 28093 MW; C9DD084F6179B41F CRC64;
 Alignment Scores:
 Pred. No.: 2,05e-70 Length: 256
 Score: 1078.00 Matches: 201
 Percent Similarity: 94.06% Conservative: 5
 Best Local Similarity: 91.78% Mismatches: 13
 Query Match: 40.00% Indels: 0
 DB: 1 Gaps: 0
 US-10-048-116-1 (1-1484) x HA2B_MOUSE (1-256)
 QY 1 ATCCGCTGAGAGAGCTGCTGCTGGGGTCTCGCCCTGAACACCATGCTCAGCCCTC 60
 DB 1 MetProArgSerArgAlaLeuLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeu 20
 QY 61 TCGGAGGTGAAGACGACATTCGAGGCCGACGCTAGGCTTCTATCGTACAACTGTTTAT 120
 DB 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyThrTyrglyIleSerValTyr 40
 QY 121 CAGTCTCTGGAGACATTCGCCAGTACACATGAATTTGATGCTGATGATGTTCTAT 180
 DB 41 GlnSerProGlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyr 60
 QY 181 GTGGACTTGGATAAGAAAGAACTCTCGAGGCTTCCTGAGTTTGGCCAAATGATGATC 240
 DB 61 ValAspLeuAspGlyGlyGlnValTyrMetLeuProGluPheGlyGlnLeuAlaSer 80
 QY 241 TTTGAGCCCAAGGTGGACTGCAAAACATAGCTGCAAAACACACAACTTGGGAATCTTG 300
 DB 81 PheAspProGlnGlyGlyLeuGlnAsnIleAlaValValIshshsnLeuGlyValLeu 100
 QY 301 ACTAAGAGCTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCAACGAGCTGTGTTCCCC 360
 DB 101 ThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
 QY 361 AGTCCCTCTGCTGCTGGTCAACCCAGCTACCACTTATCTGCTTTTGGCAACATCTTC 420
 DB 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
 QY 421 CCACCTGTGATCAACATCAATGCTGGCTCAGAAATAGCAAGTCAGTCACACGCGCTTAT 480
 DB 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValAlaAspGlyValTyr 160
 QY 481 GAGACAGCTTCTCTGCTCAACCGTGACCATCTCTTCCCAACAGCTGTCTTATCTCACCTTC 540
 DB 161 GluThrSerPhePheValAsnArgAspTyrSerPheHisLysLeuSerTyrLeuThrPhe 180
 QY 541 ATCCCTTCTGATGATGACATTTATGCTCAAGGTGGAGCTGGGCTGGAGGAGCGG 600
 DB 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
 QY 601 GTTCTGAAACACTGGGAACCTGAGATTCAGGCCCTCATGAGAGCTGACAGAACT 657
 DB 201 ValLeuLysHisTrpGluProGluLeuProAlaProMetSerGluLeuThrGluThr 219
 RESULT 13
 HA2K_MOUSE
 ID HA2K_MOUSE STANDARD; PRT; 256 AA.
 AC P01910;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE H-2 class II histocompatibility antigen, A-K alpha chain precursor.
 GN Name=H2-Aa;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=8314188; PubMed=3137158;
RA Bishop G.A., McMillan M.S., Haughton G., Frelinger J.A.;
RT "Signaling to a B-cell clone by Bk, but not Ak, does not reflect
RL alteration of Ak genes.";
RN Immunogenetics 28:184-192(1988).
RP [2]
RN SEQUENCE OF 4-256 FROM N.A.
RX MEDLINE=8316963; PubMed=6300851;
RA Benoit C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;
RT "The murine Ia alpha chains, E alpha and A alpha, show a surprising
RL degree of sequence homology.";
RN Proc. Natl. Acad. Sci. U.S.A. 80:534-538(1983).
RP [3]
RN SEQUENCE OF 24-256 FROM N.A.
RX MEDLINE=8519610; PubMed=2581258;
RA Landais D., Matthes H., Benoit C., Mathis D.;
RT "A molecular basis for the Ia.2 and Ia.19 antigenic determinants.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:2930-2934(1985).
RP [4]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 27-208.
RX MEDLINE=9818797; PubMed=9529148; DOI=10.1016/S1074-7613(00)80536-1;
RA Fremont D.H., Monnaie D., Nelson C.A., Hendrickson W.A., Unanue E.R.;
RT "Crystal structure of I-Ak in complex with a dominant epitope of
RL lysozyme.";
RN Immunity 8:305-317(1998).
CC -----
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DR EMBL; M21931; AAA39636.1; -.
DR EMBL; V00832; CAA24215.1; -.
DR EMBL; M11357; AAA39613.1; -.
DR PIR; A02217; HLMSAA.
DR PIR; I54447; I54447.
DR PDB; 1D9K; X-ray; C/G=27-209.
DR PDB; 1IAK; X-ray; A=24-222.
DR PDB; 1JL4; X-ray; A=31-208.
DR MGD; MGI:95895; H2-Aa.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00993; MHC_II_alpha; 1.
DR SMART; SM00407; IGCL; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR 3D-structure; Glycoprotein; MHC II; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 256
FT H-2 class II histocompatibility antigen,
FT A-K alpha chain.
FT DOMAIN 24 111
FT DOMAIN 112 205
FT DOMAIN 206 218
FT TRANSMEM 219 241
FT DOMAIN 242 256
FT DISULFID 134 190
FT CARBOHYD 145 145
FT STRAND 31 42
FT TURN 43 45
FT TURN 46 53
FT TURN 54 55
FT TURN 56 62
FT TURN 63 66
FT TURN 67 70
FT STRAND 73 77
FT HELIX 78 78
FT TURN

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FT STRAND 80 80
FT HELIX 83 104
FT TURN 105 105
FT STRAND 115 120
FT TURN 126 127
FT STRAND 130 139
FT STRAND 145 150
FT TURN 151 152
FT STRAND 153 154
FT TURN 157 158
FT STRAND 159 161
FT STRAND 165 166
FT TURN 168 169
FT STRAND 172 180
FT STRAND 188 193
FT TURN 195 196
FT STRAND 201 205
SQ SEQUENCE 256 AA; 28351 MW; 78E7D4A33CCE4582 CRC64;

Alignment Scores:
Pred. No.: 3.4e-70 Length: 256
Score: 1075.00 Matches: 203
Percent Similarity: 93.61% Conservative: 2
Best Local Similarity: 92.69% Mismatches: 14
Query Match: 39.89% Indels: 0
DB: 1 Gaps: 0

```

```

US-10-048-116-1 (1-1484) x HA2K_MOUSE (1-256)

QY 1 ATCCGTCGACGAGCTCTGATTCGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 60
DB 1 MecProArgSerArgAlaLeuLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeu 20
QY 61 TGGCGAGGTGAAGACGACATTTAGGCGCGACCATGAGGCTTCTATGTTGTACAACCTGTTTAT 120
DB 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyr 40
QY 121 CAGTCTCTGGAGACATTTGCCAGTACACATGAATTTGATGGTGTAGTGTCTTAT 180
DB 41 GlnSerProGlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyr 60
QY 181 GTGGACTTGGATAAGAGAAACTGTCTGGAGGCTTCTCGAGTTTGGCCAAATTCATCTC 240
DB 61 ValAspLeuAspIleGlyGlnTyrValTyrPheLeuProGluPheAlaGlnLeuArgArg 80
QY 241 TTTGAGCCCAAGGTGGAGTGCAGAAACATAGTGCAGAAAAACACACACTTTGGGAATCTTG 300
DB 81 PheGluProGlnGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGluLeu 100
QY 301 ACTAAGAGGTCAAATTTCCACCCAGCTACCAATAGGCTCTCAAGGACTGTGTTCCCTC 360
DB 101 ThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACACCTTATCTGCTTTGTGGACAACATCTTC 420
DB 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
QY 421 CCACCTGTGTATCAACATCAGTGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
DB 141 ProProValIleAsnIleThrTyrPheArgAsnSerLysSerValThrAspGlyValTyr 160
QY 481 GAGACAGCTTCTCGTCAACCGTGACCATCTCTCCCAAGCTGTCTTATCTCACCCTTC 540
DB 161 GluThrSerPhePheValAsnArgAspTyrSerPheHisLysLeuSerTyrLeuThrPhe 180
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGTGGAGCACTGGGGCCCTGGAGAGCCG 600
DB 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTyrPheGlyLeuGluPro 200
QY 601 GTTCTGAACACTGGGAACCTGAGATTCCAGCCCCCATGTGACAGCTGTACAGAACT 657
DB 201 ValLeuLysHisTyrPheGluProGluIleProAlaProMetSerGluLeuThrGluThr 219

```



```
QY 70 GAAGACGACATTGAGCCGACCGTAGGCTTCTATGGTACAACTGTTATCATGCTCTCCT 129
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22 GluAspAspIleGluAlaAspHisValAlaPheTyrGlyIleSerValTyrGlnSerPro 41
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 130 GGAACATTGGCCAGTACACACATGATTTGATGGTGTGATGAGTTGTTCTATGTGGACTTG 189
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
42 GlyAspIleGlyGlnTyrPheGluPheAspGlyAspGluLeuPheTyrValAspLeu 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 190 GATAAGAAGAAAACCTGCTGGAGGCTTCTCTAGTGTGGCCAATTGATATACTCTTTGAGCCC 249
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 AspLysLysGluThrValTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspPro 81
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 250 CAAAGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGAGG 309
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 GlnGlyGlyLeuGlnGluIleAlaThrGlyLysTyrAsnLeuGluIleLeuIleLysAsp 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 310 TCAGATTTCCACCCAGCTACCATGAGGCTCCTCAAGCGACTGTGTCCCAAGTCCCT 369
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
102 SerAsnPheThrProAlaAlaAsnGluAlaProGlnAlaThrValPheProLysSerPro 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 370 GTGCTGCTGGGTGAGCCCAACCCCTTATCTGCTTTGTGGACAAACATCTTCCACCTGTG 429
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
122 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProVal 141
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 430 ATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGCGCTTTATGAGACCAGC 489
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
142 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer 161
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 490 TTCCTGCTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTTCT 549
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
162 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer 181
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 550 GATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGAGGAGCGGTTCTGAAA 609
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
182 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 201
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 610 CACTGGGAACCTGAGATTCCAGCCCCCATGTCTAGAGCTGACAGAAACT 657
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
202 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: June 16, 2005, 02:50:45
Job time : 291.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 16, 2005, 01:40:32 ; Search time 60 Seconds
(without alignments)
4759.523 Million cell updates/sec

Title: US-10-048-116-1

Perfect score: 2695

Sequence: 1 atgcgctgcagcagagctct.....ttctccgagctccgggtaa 1484

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DRV=xlp
-Q/csp2_1/USPTO_spool_p/US10048116/runat 15062005 125142 29764/app_query.fasta_1.1671
-DB=PIR -QPM=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10048116 @CGN 1.1 80 @runat 15062005 125142 29764 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319.5	49.0	469	2	S37483
2	1317	48.9	446	2	S40295
3	1313.5	48.7	330	1	G2MSA
4	1313.5	48.7	399	1	G2MSAM
5	1182	43.9	256	2	HLMSA2
6	1075	39.9	256	2	I54447
7	1075	39.9	258	1	HLMSAA
8	1057	39.2	254	2	S11649
9	1037	38.5	335	1	G2MSAB
10	1012.5	37.6	405	1	G2MSBM
11	1010	37.5	474	1	G2MS11
12	1006	37.3	475	2	S01321
13	1000	37.1	233	2	I79357
14	996	37.0	233	2	I79358

ALIGNMENTS

RESULT 1

S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.52e-84 Length: 469
Score: 1319.50 Matches: 283
Percent Similarity: 60.96% Conservative: 23
Best Local Similarity: 56.37% Mismatches: 71
Query Match: 48.96% Indels: 125
DB: 2 Gaps: 13

US-10-048-116-1 (1-1484) x S37483 (1-469)

QY	100	TTCTATGGTACAACTGTTTATCAGTCTCTCTGGAGAC-----ATTGGC-----	141
DB	51	TyrTyrIleAsnTrpVallysGlnLysProGlyLeuLysTrpIleGlyTrpIle	70
QY	142	-----CAGTACACACATGAATTTGATCGTGCATGATGTTGTTCTAT	180
DB	71	TyrProAlaSerGlyAsnThrLysTyrAsnGluAsnPhenylsGlyAlaThrLeuThr	90
QY	181	GTGGACTTGGATAAGAAGAAACTGTCTGGAGGCTTCCTGAGTTT-----	225

```
Db 91 ValAspThrSerSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSerGluAspThr 110
QY 226 -----GGCCAAATTCATACTCTTTGAGCCC 249
Db 111 AlaValTyrPheCysAlaArgAlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGly 130
QY 250 CAAGGTGAGCTGCTGCAAGAAACACAACTTGGGAATCTTGACTAAGAGG 309
Db 131 GlnGlyThrThrLeuThrValSerSerAlaLys ----- 141
QY 310 TCAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCGACTGTGTTCCCAAGTCCCT 369
Db 142 -----ThrThrAlaPro-----SerValTyrProLeuAlaPro 152
QY 370 GTG-----CTGCTGGGTACGCCCAACACCTTATCTCTTGTGGGCAACATCTTC 420
Db 153 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 172
QY 421 CCACCTGTGATCAACATCACATGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTAT 480
Db 173 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 189
QY 481 GAGACCAGCTTCTCTCGTCAACCGTGACCATTCCTTCCACAACTGCTCTTATCTCACCTTC 540
Db 190 -----HisThrPheProAlaVal----- 195
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGAGCG 600
Db 196 -----LeuGlnSerAspLeuTyrThrLeuSer----- 204
QY 601 GTTCTGAACACTCGGAACCTGAGATTCACGCCCCCATGTCAGAGCTGCACAGAACTGGA 660
Db 205 -----SerSerValThrValThr--- 210
QY 661 GGTGGAGATCCACTACACTTCCATCAGCTCAGCTCGAAAGAGCTCCAGGCCCTGGAG 720
Db 211 -----SerSerThr----- 213
QY 721 AAGGAAATGCACAGCTGGAAATGGAGTTGGAAGCTGGAAGAAAGAACTGGCTCAGGCA 780
Db 214 -----TrpSerGlnSerIleThrCysAsnValAlaHisPro 226
QY 781 GCATCT-----GAGCCAGAGGGCCCAACATCAAGCCCTGT 816
Db 227 AlaSerSerThrLysValAspLysIleGluProArgGlyProThrIleLysProCys 246
QY 817 CCTCATGCAATGCCAGCACCTAACCTCTTGGGTGGACCATCCGCTCTTCATCTCCCT 876
Db 247 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 266
QY 877 CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGTGGTGTG 936
Db 267 ProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 286
QY 937 GATGTGCGAGGATGACCCAGATGCAGATCAGCTGGTGTGTCACACAGCTGGAAGTA 996
Db 287 AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnValGluVal 306
QY 997 CACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCAGT 1056
Db 307 HisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer 326
QY 1057 GCCCTCCCATCCAGCACAGGACTGGATGAGTGGCGAAGGATTCAAATGCAAGGTCAC 1116
Db 327 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 346
QY 1117 AACAAAGACCTCCAGCGGCCCATCGAGAGACCATCTCAAAACCCAAAGGTCAGTAAGA 1176
Db 347 AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 366
QY 1177 GCTCCACAGGTATATGTCTTCCCTCCACCAAGAGAGATGACTAAGAAACAGGTCAC 1236
Db 367 AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr 386
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QY 1237 CTGACCTGCATGTCACAGACTTCATGCTGAACAGATTTACGTGGAGTGCACCAAC 1296
Db 387 LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn 406
QY 1297 GGGAAAACAGAGCTAAACTACAAGAACACTGAACAGCTCCTGGACTCTGATGGTTCTTAC 1356
Db 407 GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr 426
QY 1357 TTCATGTACACGACGTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCC 1416
Db 427 PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer 446
QY 1417 TGTTCAGTGTCTCCAGAGGCTCTGCACAATCACACAGACTAAGAGCTTCTCCGAGCT 1476
Db 447 CysSerValValHisGluGlyLeuHisAsnHisThrThrLysSerPheSerArgThr 466
QY 1477 CCGGGT 1482
Db 467 ProGly 468

RESULT 2
S40295
I; gamma-2a chain (mAb735) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C; Accession: S40295
R; Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A; Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A; Reference number: S40295
A; Accession: S40295
A; Molecule type: protein
A; Residues: 1-446 <KLE>
A; Cross-references: UNIPROT:Q99L25
C; Genetics:
A; Map position: 12
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F; 1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F; 1-117/Domain: V-D-J region <VDJ>
F; 118-446/Domain: C region <CHR>
F; 118-214/Domain: C1 region <CH1>
F; 215-230/Region: hinge
F; 231-340/Domain: C2 region <CH2>
F; 341-446/Domain: C3 region <CH3>
F; 360-427/Domain: immunoglobulin homology <IMM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 22-96,148-199,261-321,367-425/Disulfide bonds: #status predicted
F; 132/disulfide bonds: interchain (to light chain) #status predicted
F; 224,227,229/Disulfide bonds: interchain #status predicted
F; 237/binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:
Pred. No.: 3,75e-84 Length: 446
Score: 1317.00 Matches: 280
Percent Similarity: 63.52% Conservative: 30
Best Local Similarity: 57.38% Mismatches: 78
Query Match: 48.87% Indels: 100
DB: 2 Gaps: 12

US-10-048-116-1 (1-1484) x S40295 (1-446)
QY 100 TTCATGTGTAACACTGTTTATCAGTCTCTGGAGAC-----ATTGGC----- 141
Db 32 TyrTyrIleHisTrpValLysGlnArgProGlyGluLeuGluTrpIleGlyTrpIle 51
QY 142 -----CAGTACACATGATTTGATGGTGTATGATGATGTTCTAT 180
Db 52 TyrProGlySerGlyAsnThrLysTyrAsnGluLysPheLysGlyLysAlaThrLeuThr 71
QY 181 GTGCACTTGGATAAAGAAAGAACTGTCTGGAGGCTTCTCGATTT-----GGCAA 231
Db 181
```


F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.: 6,42e-84 Length: 330
Score: 1313.50 Matches: 267
Percent Similarity: 71.03% Conservative: 15
Best Local Similarity: 67.25% Mismatches: 36
Query Match: 48.74% Indels: 79
DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x G2MSA (1-330)

```

Qy 325 GCTACCAATGAGGCTCTCAAGCAGCTGTGTTCCTCCCAAGTCCCTGTG-----CTG 375
D 1 AlalysThrThrAlaPro-----SerValTyrProLeuAlaProValCysGlyAspThr 18
Qy 376 CTGGGTGAGCCCAACACCTTATCTGCTTTGTGGACAACATCTTCCACCTGTGATCAAC 435
D 19 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr 38
Qy 436 ATCATGGTTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACCAGCTTCTC 495
D 39 LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal----- 50
Qy 496 GTCAACGTGACCATTCCTTCCACAGCTGTCTTATCTCACCTTCATCCCTTCTGTGATGAT 555
D 51 -----HisThrPheProAlaVal-----LeuGlnSer 59
Qy 556 GACATTTATGACTGCAAGGTGGACACTGGGGCCTGGAGGAGCCGGTCTGAAACACTGG 615
D 60 AspleuTyrThrLeuSer----- 65
Qy 616 GAACCTGAGATTCAGCCGCCCATGCTCAGAGCTGACAGAACTGGAGGTGGAGGATCCACT 675
D 66 -----SerSerValThrValThr-----SerSer 73
Qy 676 ACAGCTCAGCTCAGCTCGAANAAGAGCTCCAGGCCCTGGAGAGGAAATGCAAG 735
D 74 Thr----- 74
Qy 736 CTGGAATGGGAGTTGCAAGCACTGGAAAGAACTGGCTCAGGCAGCATCT----- 786
D 75 -----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLys 92
Qy 787 -----GAGCCAGAGGGCCCAATCAAGCCCTGCTCTCCATGCAAAATGC 831
D 93 ValAspLysLysIleGluProArgGlyProThrIleLysProCysProCysLysCys 112
Qy 832 CCAGCAGCTAACCTCTTGGGTGGACCATCGCTCTTCATCTTCCCTCCAAAGATCAAGAT 891
D 113 ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 132
Qy 892 GTACTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGGATGTGAGCGAGAT 951
D 133 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 152
Qy 952 GACCCAGATGCCAGATCAGCTGGTTTGTGAACAACTGGAGGTACACAGCTCAGACA 1011
D 153 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 172
Qy 1012 CAACCCATGAGAGGATTACAAAGTACTCTCCGGGTGGTCACTGCTCCCTCCCATCCAG 1071
D 173 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 192
Qy 1072 CACGAGCACTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACAAAGAGCTCCCA 1131
D 193 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro 212
Qy 1132 GCGCCCATGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATAT 1191
D 213 AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr 232

```

```

Qy 1192 GTCTTGCTCCACCAGGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTC 1251
D 233 ValLeuProProGluGluMetThrLysLysGlnValThrLeuThrCysMetVal 252
Qy 1252 ACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAACGGGAAACAGAGCTA 1311
D 253 ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu 272
Qy 1312 AACTACAAGAACACTGAACACAGCTCCTGGACTCTGATGGTGTCTTACTTTCATGTACAGCAAG 1371
D 273 AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys 292
Qy 1372 CTGAGAGTGAAGAAGAACTGGGTGGAAGAAATAAGTACTCTCTTTCAGTGTGTCAC 1431
D 293 LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis 312
Qy 1432 GAGGGTCTGCACATCAATCACACAGCACTAAGAGCTTCTCCCGGACTCCGGGT 1482
D 313 GluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGly 329

```

RESULT 4

G2MSAM
Ig gamma-2a chain C region, membrane-bound form - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Feb-1984 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C/Accession: A02154; B32657; I57809
R/Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A/Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul
A/Reference number: A02154; MUID:82222190; PMID:6283537
A/Accession: A02154
A/Molecule type: DNA
A/Residues: 329-399 <YAM>
A/Cross-references: UNIPROT:P01865; GB:J00471
A/Note: the sequence was determined from the germline gene
R/Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A/Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and ev
A/Reference number: A32657; MUID:81198976; PMID:6262729
A/Accession: B32657
A/Molecule type: DNA
A/Residues: 1-329 'K' <YA2>
R/Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A/Title: Sequence and polyadenylation site determination of the murine immunoglobulin ga
A/Reference number: I57809; MUID:90097953; PMID:2513486
A/Accession: I57809
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 373-399 <RES>
A/Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C/Comment: The sequence of residues 1-328 was assumed to be identical with the correspond
C/Comment: Cell lines producing IGG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C/Genetics:
C/Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F/137-206/Domain: immunoglobulin homology <YMM>
F/346-363/Domain: transmembrane #status predicted <TMM>
F/364-399/Domain: intracellular #status predicted <INT>
F/180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 6,52e-84 Length: 399
Score: 1313.50 Matches: 267
Percent Similarity: 71.03% Conservative: 15
Best Local Similarity: 67.25% Mismatches: 36
Query Match: 48.74% Indels: 79
DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x G2MSAM (1-399)

QY	325	GCTACCAATGAGGCTCTCTCAAGCAGCATGTGTCTCCCAAGTCCCTCTGTG-----CTG	375
Db	1	AlaIysThrAlaPro-----SerValTyrProLeuAlaProValCysGlyAspThr	18
QY	376	CTGGGTGAGCCCAACACCCCTTATCTGCTTGTGTGGACCAACATCTTCCACACCTGTGATCAAC	435
Db	19	ThrGlySerSerValThrLeuGlyCysLeuValIysGlyTyrPheProGluProValThr	38
QY	436	ATCACATGGCTCAGAAATAGCAAGTCAAGTCAACAGACGGCGTTTATGAGACCAAGCTTCCTC	495
		:::	
Db	39	LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal-----	50
QY	496	GTCNAACGCTGACCATCTCTTCCCAACAGCTGCTTATCTCACCTTCATCCCTTCTGTGATGAT	555
Db	51	-----HisThrPheProAlaVal-----LeuGlnSer	59
QY	556	GACATTTATGACTGCAAGGTGGAGCACTGGGGCCCTGGAGGAGCGGTTCTGAAACACATGG	615
Db	60	AspLeuTyrThrLeuSer-----	65
QY	616	GAACCTGAGATTTCAGGCCCCCATGTCAGAGCTGCACAGAAACTGGAGGTGGAGGATCCACT	675
Db	66	-----SerSerValThrValThr-----SerSer	73
QY	676	ACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCAGGCCCCCTGGAGAGGAAAAATGCACAG	735
Db	74	Thr-----	74
QY	736	CTGGAATGGAGTTGTCAAGCACTGCAAAAAGCACTGGCTCAGGCAGCATCT-----	786
Db	75	-----TrpSerGlnSerIleThrCysAsnValAlaHisProIleAsSerSerThrLys	92
QY	787	-----GAGCCGAGAGGCCCAACATCAAGCCCTCTCTCCATGCAAAATGC	831
Db	93	ValAspLysIysIleGluProArgGlyProThrIleLysProCysProCysLysCys	112
QY	832	CCAGCCTTAACCTCTGGGTGGACCATCGTCTTCATCTTCCCTCAAAAGATCAAGGAT	891
Db	113	ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp	132
QY	892	GTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGAT	951
Db	133	ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp	152
QY	952	GACCCAGATGTCCAGATCAGCTGGTGTGTGAAACAACCTGGAAGTACACACAGCTCAGACA	1011
Db	153	AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr	172
QY	1012	CAAAACCATAGAGAGGATTACACAGTACTCTCCGGGTGGTGCAGTGCCTCCCATCCAG	1071
Db	173	GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln	192
QY	1072	CACCAAGACTTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCA	1131
Db	193	HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro	212
QY	1132	CGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAAGCTCCACAGGTATAT	1191
Db	213	AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr	232
QY	1192	GTCTTGCTCCACGAGAGAGAGATCAGCTAAGAAACAGGTCACTCTGACCTGCGATGGTC	1251
Db	233	ValLeuProProProGluGluMetThrLysLysGlnValThrLeuThrCysMetVal	252
QY	1252	ACAGCTTCATCGCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAAACAGAGCTA	1311
Db	253	ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu	272
QY	1312	AACCTACAAGAACTGAACCAAGTCCCTGGACTCTGATGGTCTTACTTCACTGTGTACGCAAG	1371
Db	273	AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys	292

QY 1372 CTGAGAGCTGGAAAGAGAACTGGTGGGAAGAAATAGCTACTCCTGTTCAGTGGTCCAC 1414
 Db 293 LeuArgValGluuIysLysAsnIrpValGluArgAsnSerIyrSerCysSerValValHis 312
 QY 1432 GAGGGTCTGCACAAATCAACACAGACTAAGAGCTTCTCCCGAGATCCGGGT 1482
 Db 313 GluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGly 329
 RESULT 5
 H1MSA2
 L2 Class II histocompatibility antigen A-d alpha chain precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
 C;Accession: A02219; S20786
 R;Benoit, C.O.; Mathis, D.J.; Kanter, M.R.; Williams II, V.E.; McDevitt, H.O.
 Cell 34, 169-177, 1983
 A;Title: Regions of allelic hypervariability in the murine A-alpha immune response
 A;Reference number: A90837; MUID:63285339; PMID:6309407

RESULT 5

HLMSA2

H-2 class II histocompatibility antigen A-d alpha chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C:Accession: A02219; S20786

R:Benoist, C.O.; Mathis, D.J.; Kanter, M.R.; Williams II, V.E.; McDevitt, H.O.

Cell 34, 169-177, 1983

A:Title: Regions of allelic hypervariability in the murine A-alpha immune response gene.

A:Reference number: A90837; MUID:83285339; PMID:6309407

A:Accession: A02219

A:Molecule type: mRNA

A:Residues: 1-256 <BEN>

A:Cross-references: UNIPROT:P04228; GB:K01923; NID:g199449; PIDN:AAA39615.1; PID:g199450

R:Nygard, N.R.; McCarthy, D.M.; Schiffenauer, J.; Schwartz, B.D.

submitted to the EMBL Data Library, August 1990

A:Description: Nucleotide sequence of MHC class II genes in the NZB mouse.

A:Reference number: S20786

A:Accession: S20786

A:Molecule type: DNA

A:Residues: 34-106 <NYG>

A:Cross-references: EMBL:X54425; NID:G53093; PIDN:CAA38297.1; PID:G53094

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

C:Keywords: heterodimer; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-256/Product: H-2 class II histocompatibility antigen A-d alpha chain #status predicted

F:24-111/Domain: alpha-1 <EX1>

F:112-205/Domain: alpha-2 <EX2>

F:127-192/Domain: immunoglobulin homology <IMM>

F:206-218/Domain: connecting peptide #status predicted <CCP>

F:219-244/Domain: transmembrane #status predicted <TMW>

F:245-256/Domain: intracellular #status predicted <INT>

F:134-190/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.:	9,41e-75	Length:	256
Score:	1182.00	Matches:	219
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	43.86%	Indels:	0
DB:	1	Gaps:	0

US-10-048-116-1 (1-1484) x HLMSA2 (1-256)

Alignment Scores:	
Pred. No.:	9,418-75
Score:	1182.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	43.86%
DB:	1
Length:	256
Matches:	219
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-048-116-1 (1-1484) x HLMSA2 (1-256)

Qy	1	ATGCGCTGCAGCAGAGCTCTGATTCTGGGGGTCTCTCGCCCTGAACACCATGCTCAGCCTC	60
Db	1	MetProCysSerArgAlaLeuIleuGlyValLeuAlaLeuAenThrMetLeuSerLeu	20
Qy	61	TGCGGAGGTGAAGACGACATTGAGCGCCACCACTAGCGTCTTATGGTGACAACTGTTTAT	120
Db	21	CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr	40
Qy	121	CAGTCTCTGGAGACATTGGCCAGGTACACATGAAATTTGATGGTGATGAGTTGTTCTTAT	180
Db	41	GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr	60
Qy	181	GTGGACTTGGATAAGACAGAAACTGTCTGGAGGCTCTCTGAGTTTGGCCAAATGATACTC	240
Db	61	ValAspLeuAspLeuAspLeuValThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu	80
Qy	241	TTTGAGCCCCAAGGTGGAGCTCAAAACATAGCTCGAGAAAAACAACTTTGGGAATCTTG	300
Db	81	PheGluProGlnGlyGlyLeuGlnAsnIleAlaGluLysHisAsnLeuGlyIleLeu	100

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QY 301 ACTAAGAGGTCAAATTTACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360
Db 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACCTCTTATCTGCTTTGTGGCAACATCTTC 420
Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
QY 421 CCACCTGTGATCAACATCAGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
QY 481 GAGACCACTTCTCGCTCAACCGTGACCATTCCTTCCACAGCTGCTTATCTCACCTTC 540
Db 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGAGCGG 600
Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
QY 601 GTTCTGAAACTGGGAACCTGAGATTCAGACCCCATGTGTCAGAGCTGACAGAAACT 657
Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
RESULT 6
154447
Gene MHC H2-I-A-alpha chain protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I54447
R:Bishop, G.A.; McMillan, M.S.; Houghton, G.; Frelinger, J.A.
Immunogenetics 28, 184-192, 1988
A:Title: Signaling to a B-cell clone by E-k, but not A-k, does not reflect alteration of
A:Reference number: I54447; MUID:88314188; PMID:3137158
A:Accession: I54447
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-256 <RES>
A:Cross-references: UNIPROT:P01910; GB:M21931; NID:g199493; PIDN:AAA39636.1; PID:g199494
C:Genetics:
A:Gene: MHC-H2-I-A-alpha
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:127-192/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 2,75e-67 Length: 256
Score: 1075.00 Matches: 203
Percent Similarity: 93.61% Conservative: 2
Best Local Similarity: 92.69% Mismatches: 14
Query Match: 39.89% Indels: 0
DB: 2 Gaps: 0
US-10-048-116-1 (1-1484) x I54447 (1-256)
QY 1 ATGCCGTGCAGCAGACTCTGATTCGGGGTCTCGCCCTGACACCATGCTCAGCCTC 60
Db 1 MetBroArgSerArgAlaLeuIleGlyValLeuAlaLeuThrMetLeuSerLeu 20
QY 61 TGGCGAGGTGAAGACGACATTCAGGCGCCACACGATGGCTTCTATGCTACAACTGTTTAT 120
Db 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyr 40
QY 121 CAGTCTCTGAGACATTTGGCCAGCTACACATGAATTTGATGTGATGATGTTCTTAT 180
Db 41 GlnSerProGlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyr 60
QY 181 GTGCACTTGGATAAGAGAAACTGCTGGAGGCTCTCTGAGTTTGGCCATTCATCATC 240
Db 61 ValAspLeuAspLysLysGluThrValTrpMetLeuProGluPheAlaGlnLeuArg 80
QY 241 TTTGAGCCCCAAGGTGACCTGCAAAACATAGCTGCAGAAACAAACAACTTTGGGAATCTTG 300
Db 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGluIleLeu 100
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QY 301 ACTAAGAGGTCAAATTTACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360
Db 101 ThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420
Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
QY 421 CCACCTGTGATCAACATCAGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
QY 481 GAGACCACTTCTCGCTCAACCGTGACCATTCCTTCCACAGCTGCTTATCTCACCTTC 540
Db 161 GluThrSerPhePheValAsnArgAspTyrSerPheHisLysLeuSerTyrLeuThrPhe 180
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGAGCGG 600
Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
QY 601 GTTCTGAAACTGGGAACCTGAGATTCAGACCCCATGTGTCAGAGCTGACAGAAACT 657
Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
RESULT 7
HLMSAA
H-2 class II histocompatibility antigen A alpha chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A02217, I59023; A32510
R:Benoist, C.O.; Mathis, D.J.; Kanter, M.R.; Williams II, V.B.; McDevitt, H.O.
Proc. Natl. Acad. Sci. U.S.A. 80, 534-538, 1983
A:Title: The murine Ia alpha chains, E-alpha and A-alpha, show a surprising degree of se
A:Reference number: A93967; MUID:83169693; PMID:6300851
A:Accession: A02217
A:Molecule type: mRNA
A:Residues: 1-258 <BEN>
A:Cross-references: UNIPROT:P01910
A:Experimental source: clone pAAC6
R:Landais, D.; Matthes, H.; Benoist, C.O.; Mathis, D.
Proc. Natl. Acad. Sci. U.S.A. 82, 2930-2934, 1985
A:Title: A molecular basis for the Ia.2 and Ia.19 antigenic determinants.
A:Reference number: I59023; MUID:85190610; PMID:2581258
A:Accession: I59023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 26-258 <RES>
A:Cross-references: GB:M11357; NID:g199445; PIDN:AAA39613.1; PID:g387459
R:Sharma, S.; King, L.B.; Corley, R.B.; Maki, R.
Immunol. Invest. 16, 425-436, 1987
A:Title: Comparative sequence analysis of cDNA clones encoding I-A molecules of the CH12
A:Reference number: A91752; MUID:88085327; PMID:3500915
A:Accession: A32510
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 18-258 <SHA>
C:Comment: Residues 1-25 are part of the signal sequence.
C:Comment: Residues 26-113, 114-207, and 208-258 are the first and second extracellular
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:129-194/Domain: immunoglobulin homology <IMM>
F:107,147/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:136-192/Disulfide bonds: #status predicted
Alignment Scores:
Pred. No.: 2,76e-67 Length: 258
Score: 1075.00 Matches: 202
Percent Similarity: 94.01% Conservative: 2
Best Local Similarity: 93.09% Mismatches: 13
Query Match: 39.89% Indels: 0
DB: 1 Gaps: 0
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US-10-048-116-1 (1-1484) x HLMSAA (1-258)

QY 7 TGACAGAGAGCTCTGATTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTCTGGGA 66
Db 5 CysSerArgAlaLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeuCysGly 24
QY 67 GGTGAAGACGACATTGAGGCGGACGAGTGTCTATGGTACAACTGTTTATCAGTCT 126
Db 25 GlyGluAspIleGluAlaAspHisValGlySerTyrglyIleThrValTyrglnSer 44
QY 127 CTGGGACATATGGCCAGTACACACATGAATTTGATGGTATGAGTGTCTATGGAC 186
Db 45 ProGlyAspIleGlyGlnTyThrPheGluPheAspGlyAspGluLeuPheTyValAsp 64
QY 187 TTGGATAAGAAAGAACTGTCTGGAGCTTCTGAGTTTGGCCAAATTGATCTTTGAG 246
Db 65 LeuAspIleGlyGlnTyThrValTrpMetLeuProGluPheAlaGlnLeuArgArgPheGlu 84
QY 247 CCCAAGGTGGATGCAAAACATAGCTGCGAAGAAACACAACTTGGGAATCTTTGACTAAG 306
Db 85 ProGlnGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGluIleLeuThrLys 104
QY 307 AGTCAAAATTTCCCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCCAAGTCC 366
Db 105 ArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSer 124
QY 367 CTGTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGACAAACATCTTCCACCT 426
Db 125 ProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProPro 144
QY 427 GTGATCAACATCATGGCTCAGAAATAGCAAGTCAGTCACAGCGCGGTTTATGAGACC 486
Db 145 ValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrgluThr 164
QY 487 AGCTTCTCTGTAACCGTGACCAATCTCTTCCACAGCTGCTTATCTCAGCTTCATCCCT 546
Db 165 SerPhePheValAsnArgAspTyThrPheHisLysLeuSerTyrgluThrPheIlePro 184
QY 547 TCTGATGATGACATTTATGACTCAAGGTGAGACACTGGGGCTGGAGGAGCGGTTCTG 606
Db 185 SerAspAspIleTyThrAspCysLysValGluHisTrpGlyLeuGluProValLeu 204
QY 607 AAACACTGGGAACCTGAGATTCCAGCCCTCCATGCTCAGAGCTGACAGAACT 657
Db 205 LysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 221

RESULT 8
S11649
class II histocompatibility antigen H-2-I-A-alpha NON - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: I4821; S11649
R;Acha-Orbea, H.; Scarpellino, L.
Immunogenetics 34, 57-59, 1991
A;Title: Nonobese diabetic and nonobese nondiabetic mice have unique MHC class II haplotypes
A;Reference number: I48224; MUID:91310089; PMID:1855817
A;Accession: I48421
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-254 <RES>
A;Cross-references: UNIPROT:P23150; EMBL:X52643; NID:G51526; PIDN:CAA36865.1; PID:G51527
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
C;Keywords: heterodimer
F;125-190/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 4.96e-66 Length: 254
Score: 1057.00 Matches: 198
Percent Similarity: 93.52% Conservative: 4
Best Local Similarity: 91.67% Mismatches: 14
Query Match: 39.22% Indels: 0
DB: 2 Gaps: 0

US-10-048-116-1 (1-1484) x S11649 (1-254)

QY 10 AGCAGAGCTCTGATTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTCTCGGAGGT 69
Db 2 SerArgAlaLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeuCysGly 21
QY 70 GAAGACGACATGAGGCGGACGACGAGTGTCTATGGTACAACTGTTTATCAGTCTCT 129
Db 22 GluAspAspIleGluAlaAspHisValAlaPheTyrglyIleSerValTyrglnSerPro 41
QY 130 GGAGACATTTGGCCAGTACACACATGAATTTGATGGTATGAGTGTCTATGGACTTG 189
Db 42 GlyAspIleGlyGlnTyThrPheGluPheAspGlyAspGluLeuPheTyValAspLeu 61
QY 190 GATAACAAGAAACTCTCTGGAGGCTTCTGAGTTTGGCCAAATTGATCTTTTGAGCCC 249
Db 62 AspLysLysGluThrValTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspPro 81
QY 250 CAAAGTGGACTGCAAAACATAGCTGCGAAGAAACACAACTTGGGAATCTTTGACTAAGAGG 309
Db 82 GlnGlyGlyLeuGlnGluIleAlaThrGlyLysTyAsnLeuGluIleLeuIleLysAsp 101
QY 310 TCAAAATTTCCCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCCAAGTCCCT 369
Db 102 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 121
QY 370 GTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGACAAACATCTTCCACCTGTG 429
Db 122 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProVal 141
QY 430 ATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGCGCGGTTTATGAGACCAGC 489
Db 142 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrgluThrSer 161
QY 490 TTCCTCGTCAACCGTGACCAATCTCTTCCACAGCTGCTTATCTCAGCTTCATCCCTTCT 549
Db 162 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrgluThrPheIleProSer 181
QY 550 GATGATGACATTTATGACTCAAGGTGAGGAGCTGGGGCTGGAGGAGCGGTTCTGAAA 609
Db 182 AspAspAspIleTyThrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 201
QY 610 CACTGGGAACCTGAGATTCCAGCCCTCCATGCTCAGAGCTGACAGAACT 657
Db 202 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 217

RESULT 9
G2MSAB
Ig gamma-2a chain C region, secreted form (allele b) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A02153; A32656
R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and IgG2b heavy chain C regions
A;Reference number: A02153; MUID:82037861; PMID:6170065
A;Accession: A02153
A;Molecule type: mRNA
A;Residues: 1-335 <SCH>
A;Cross-references: UNIPROT:P01864; GB:J00479
A;Experimental source: strain C57BL/6
R;Dognin, M.J.; Lauwereys, M.; Stroobergs, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain C region and gamma 2b heavy chain C region
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
A;Molecule type: protein
A;Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>
C;Comment: Lys-335 is removed posttranslationally.
C;Comment: The sequence differs from that of the allele, from BALB/c mice, at 15% of the amino acids
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Score:	1012.50	Matches:	210
Percent Similarity:	63.59%	Conservative:	38
Best Local Similarity:	53.85%	Mismatches:	69
Query Match:	37.57%	Indels:	73
DB:	1	Gaps:	10
US-10-048-116-1 (1-1484) x G2MSB (1-405)			
QY	349	ACTGTGTTCCCAAGTCCCT	-----GTCTGCTGGTGCAGCCCAACACCCCTTATC 399
Db	7	SerValTyrProLeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGly 26	
QY	400	TGCTTTGTGGACAACATCTTCCACCTGTGATCAACATCATCATGGCTCAGAAATAGCAAG 459	
Db	27	CysLeuValLysGlyThrProGluSerValThrValTrp-----AsnSerGly 44	
QY	460	TCAGTCACAGCGGCTTTATGAGACGAGCTTCTCGTCACCGTGACCATCTCTTCCAC 519	
Db	45	SerLeuSerSerSerValHis-----ThrPheProAlaLeuLeuGlnSerGlyLeuTyr 62	
QY	520	AAGCTGCTTATCTCACCTTCATCTCTCTCTGAT-----GATGACATTTATGACTGC 570	
Db	63	ThrMetSerSerSerValThrValProSerSerThrTrpProSerGlnThrValThrCys 82	
QY	571	AAGGTGGAGCACTGGGGCCCTGGAGGAGCCGGTTCTCAAAACACTGGGAACCTGAGATTCCA 630	
Db	83	SerValAlaHis-----Pro 87	
QY	631	GGCCCATGTGCAGCTGACAGAACTGGAGGTGGAGGATCCACTACAGCTCATCAGCT 690	
Db	88	Ala-----SerSerThrThr----- 92	
QY	691	CAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAATGCACAGCTGGAAATGGGGATTG 750	
Db	92	----- 92	-----
QY	751	CAAGCACTGGAAAGGAAGTGGCTCAGCGAGCATCTGAGCCGAGGGGCC-----ACA 804	
Db	93	-----ValAspLysLysLeu-----GluProSerGlyProIleSerThr 105	
QY	805	ATCAAGCCCTGCTCTCATGC-----AAATGCCAGCAGCTAACCTCTTGGGT 852	
Db	106	IleAsnProCysProCysLysGluCysHisLysCysProAlaProAsnLeuGluGly 125	
QY	853	GGACCATCGTCTTCTCTCTCTCCCTCAAGATCAAGATGTACTCATGATCTCCCTGAGC 912	
Db	126	GlyProSerValPheIlePheProProAsnIleLysAspValLeuMetIleSerLeuThr 145	
QY	913	CCCATAGTCATGTGTGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGC 972	
Db	146	ProLysValThrCysValValValAspValSerGluAspAspProAspValGlnIleSer 165	
QY	973	TGTTTGTGAACACGTGGAAGTACACAGCTCAGACACAAACCATAGAGGATTAC 1032	
Db	166	TrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisargGluAspTyr 185	
QY	1033	AACAGTACTCTCCGGTGGTGCAGTCCCTCCCATCCAGCAGCAGCTGGATGAGTGGC 1092	
Db	186	AsnSerThrIleargValValSerThrLeuProIleGlnHisGlnAspTrpMetSerGly 205	
QY	1093	AAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCAGCGCCCATCCAGAGAACCATC 1152	
Db	206	LysGluPheLysCysLysValAsnAsnLysAspLeuProSerProIleGluargThrIle 225	
QY	1153	TCAAAACCAAGGGTCAGTAAGAGCTCCAGAGTATATGTCTTGGCTCCACCAAGAA 1212	
Db	226	SerLysIleLysGlyLeuValArgAlaProGlnValIleLeuProProAlaGlu 245	
QY	1213	GAGTACTAAGAAACAGGTCACTCTGACCTGCTGATGTCACAGCTTCATGCTGAAGAC 1272	
Db	246	GlnLeuSerArgLysAspValSerLeuThrCysLeuValValGlyPheAsnProGlyAsp 265	
QY	1273	ATTTCAGTGGAGTGGAACCAACACGGGAAAAACAGAGCTAAACTTACAAGAACACTGAACCA 1332	

Db	266	IleSerValGluTrpThrSerAsnGlyHisThrGluGluAsnTyrLysAspThrAlaPro 285	
QY	1333	GTCTGGACTGTGATGGTTCTTACTTCATGTACAGCAAGCTGAGATGGGAAAGAGAAC 1392	
Db	286	ValLeuAspSerAspGlySerTyrPheIleTyrSerLysLeuAsnMetLysThrSerLys 305	
QY	1393	TGGGTGGAAAGAAATAGTACTCTCTTCAGTGGTCCAGAGGCTTCGACATATCACCAC 1452	
Db	306	TrpGluLysThrAspSerPheSerCysAsnValArgHisGluGlyLeuLysAsnTyrTyr 325	
QY	1453	ACGACTAAGAGCTTCTCCCGGACTCCGGGT 1482	
Db	326	LeuLysLysThrIleSerArgSerProGly 335	
RESULT 11			
G2MS11			
Ig gamma-2b chain - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004			
C:Accession: S25057; A02157; A26235; A26233; A26233; A53598			
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.			
submitted to the EMBL Data Library, July 1992			
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m			
A:Reference number: S25057			
A:Accession: S25057			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-474 <PIS>			
A:Cross-references: P01866; EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827			
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.			
Nature 283, 786-789, 1980			
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from n			
A:Reference number: A02157; MUID:80120716; PMID:6766534			
A:Contents: a allele			
A:Accession: A02157			
A:Molecule type: DNA			
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>			
A:Cross-references: GB:J00461			
A:Note: the sequence was determined from the germline gene			
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.			
Science 206, 1299-1303, 1979			
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea			
A:Reference number: A26235; MUID:80081501; PMID:117548			
A:Contents: MPC 11			
A:Accession: A26235			
A:Molecule type: mRNA			
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>			
A:Note: Lys-474 is probably removed posttranslationally			
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.			
Science 206, 1303-1306, 1979			
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglot			
A:Reference number: A26233; MUID:80081502; PMID:117549			
A:Accession: A26233			
A:Molecule type: DNA			
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>			
R:Ollo, R.; Rougeon, F.			
Nature 296, 761-763, 1982			
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma			
A:Reference number: A26233; MUID:82173203; PMID:6803173			
A:Contents: b allele			
A:Accession: A26233			
A:Molecule type: DNA			
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>			
A:Cross-references: GB:J00461			
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi			
J. Biol. Chem. 269, 12345-12350, 1994			
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.			
A:Reference number: A53598; MUID:94216359; PMID:7512967			
A:Accession: A53598			
A:Status: preliminary			
A:Molecule type: protein			
A:Residues: 234-251 <KIM>			

C;Comment: The a allele sequence is shown.

C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 9,97e-63 Length: 474
Score: 1010.00 Matches: 217
Percent Similarity: 60.99% Conservativity: 41
Best Local Similarity: 51.30% Mismatches: 75
Query Match: 37.48% Indels: 90
DB: 1 Gaps: 12

US-10-048-116-1 (1-1484) x G2MS11 (1-474)

```
Qy 250 CAAGTGGAGTCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTTAAGAGG 309
Dy 129 GlnGlyThrLeuValThrValSerAlaAlaLys-----
Qy 310 TCAAAATTTCAACCCAGCTACCAATGAGCTCTCAAGGACTGTGTTCCCAAGTCCCT 369
Dy 140 -----ThrThrPro-----ProSerValThrProLeuAlaPro 150
Qy 370 -----GTGCTGTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420
Dy 151 GlyCysGlyAspThrThrGlySerSerValThrSerGlyCysLeuValLysGlyTyrPhe 170
Qy 421 CCACCTGTGATCAACATCAGATGCTCAGAAATAGCAAGTCAAGTCAAGAGGGGTTAT 480
Dy 171 ProGluSerValThrValThrTrp-----AsnSerGlySerLeuSerSerValHis 188
Qy 481 GAGACACAGCTTCTCTGTCACCGTCCATTCCTTCCACAGCTGCTTATCTCACCTTC 540
Dy 189 ThrLeuSerGlnAlaLeuLeuGlnSerGlyLeuTyrThrMetSerSerValThr--- 207
Qy 541 ATCCCTTCTGAT-----GATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTG 591
Dy 208 ValProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHis----- 224
Qy 592 GAGGAGCGGTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTGAGAGCTGACA 651
Dy 225 -----ProAla-----
Qy 652 GAAACTGGAGTGGAGATCCACTACAGCTCCATCAGCTCAGCTCGAAGAAAGAGCTCCAG 711
Dy 227 -----SerSerThrThr-----
Qy 712 GCCCTGGAGAGGAAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGAACTG 771
Dy 231 -----ValAspLysLysLeu 235
Qy 772 GCTCAGCAGCATCTGAGCCAGAGGGGCC-----ACAATCAAGCCCTGCTCTCCATGC 825
Dy 236 -----GluProSerGlyProIleSerThrIleAsnProCysProProCys 250
Qy 826 -----AAATGCCAGACCTTAACCTCTTGGTGGACCATCCGCTTCTCATCTTC 873
Dy 251 LysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPheIlePhe 270
Qy 874 CCTCCAAGATCAAGGATGACTCATGATCTCTGAGCCCCCATPAGTCAATGTGTGTG 933
Dy 271 ProProAsnIleLysAspValLeuMetIleSerLeuThrProLysValThrCysValVal 290
```

```
Qy 934 GTGGATGTGAGCGAGGATGACCCAGATGTCAGATGAGCTGCTTGTGAACAACTGGAA 993
Dy 291 ValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnValGlu 310
Qy 994 GTACACACAGCTCAGACACAAACCCATAGAGAGATTACAACTACTCTCCGGGTGCTC 1053
Dy 311 ValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArgValVal 330
Qy 1054 AGTGCCCTCCCATCCAGCACCAAGGACTGGATGAGTGGCGCAAGGAGTTCAAATGCAAGTTC 1113
Dy 331 SerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysVal 350
Qy 1114 AACAAACAAACACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTTCAGTA 1173
Dy 351 AsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLysGlyLeuVal 370
Qy 1174 AGAGTCCACAGGTATATGTTCTTGTCCCTCCACCAAGAAAGAGATGACTTAAGAAACAGTTC 1233
Dy 371 ArgAlaProGlnValTyrIleLeuProProProAlaGluGlnLeuSerArgLysAspVal 390
Qy 1234 ACTCTGACCTGATGCTCAGAGCTTCATCGCTGAAACATTTTACGTGGAGTGGACCAAC 1293
Dy 391 SerLeuThrCysLeuValValGlyPheAsnProGlyAspIleSerValGluTrpThrSer 410
Qy 1294 AACGGGAAACACAGAGCTAAACTACAAACACACTGAACCACTCTGGAGCTCTGATGTTCT 1353
Dy 411 AsnGlyHisThrGluGluAsnTyrLysAspThrAlaProValLeuAspSerAspGlySer 430
Qy 1354 TACTTCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTAC 1413
Dy 431 TyrPheIleTyrSerLysLeuAsnMetLysThrSerLysTrpGluLysThrAspSerPhe 450
Qy 1414 TCCTGTTTACTGTGTCACGAGGCTGTCACAAATCACACACAGCTTAAGAGCTTCTCCGG 1473
Dy 451 SerCysAsnValArgHisGluGlyLeuLysAsnTyrTyrLeuLysLysThrIleSerArg 470
Qy 1474 ACTCCGGGT 1482
Dy 471 SerProGly 473
RESULT 12
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IM1>
Alignment Scores:
Pred. No.: 1.9e-62 Length: 475
Score: 1006.00 Matches: 214
Percent Similarity: 62.28% Conservativity: 37
Best Local Similarity: 53.10% Mismatches: 76
Query Match: 37.33% Indels: 76
DB: 2 Gaps: 11
US-10-048-116-1 (1-1484) x S01321 (1-475)
Qy 319 ACCCCAGCTACCAATGAGGCTCCTCAAGCAGCT-----GTGTTCCCAAGTCCCT 369
```


Db 161 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLys 180

Qy 610 CACTGGGAACCTGAGATTCCAGCCCCCATGTGTCAGAGCTGACAGAAACT 657
|||||

Db 181 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 196

RESULT 14

I79358

IA-alpha polypeptide - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I79358
R:Landaig, D.; Matthes, H.; Benoist, C.O.; Mathis, D.
Proc. Natl. Acad. Sci. U.S.A. 82, 2930-2934, 1985
A:Title: A molecular basis for the Ia.2 and Ia.19 antigenic determinants.
A:Reference number: 159023; MUID:85190610; PMID:2581258
A:Accession: I79358
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
C:Superfamily: UNIPROT:P14437; GB:M11358; NID:g199465; PIDN:AAA39622.1; PID:g387462
C:Keywords: class II histocompatibility antigen; immunoglobulin homology
F:104-169/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8.89e-62 Length: 233
Score: 996.00 Matches: 183
Percent Similarity: 95.41% Conservative: 4
Best Local Similarity: 93.37% Mismatches: 9
Query Match: 36.96% Indels: 0
DB: 2 Gaps: 0

US-10-048-116-1 (1-1484) x I79358 (1-233)

Qy 70 GAAGACGACATTGAGCGGCACAGTCTGATGTTCTATGGTACAACTGTTTATCAGTCTCCT 129
|||||

Db 1 GluAspAspIleGluAlaAspHisValGlyValTyrGlyThrValTyrGlnSerPro 20

Qy 130 GGAGACATTGCCAGTACACATGAATTTGATGGTGAATGTTGTTCTATGTGGACTTG 189
|||||

Db 21 GlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyrPheTyrValAspLeu 40

Qy 190 GATAGAGAAAACGTCTGAGGCTTCTGAGTTTGGCCAAATGATCTTTTGAGCCC 249
|||||

Db 41 AspLysLysGluThrIleTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspPro 60

Qy 250 CAAGGTGACTGCAAAACATAGCTGCAGAAAACACAACTTGGGAATCTTGACTAAAGAG 309
|||||

Db 61 GlnGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGlyIleLeuThrLysArg 80

Qy 310 TCAATTTTCAACCGTACCAATGAGCTCCTCAAGCGACTGTGTTCCCAAGTCCCT 369
|||||

Db 81 SerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 100

Qy 370 GTGCTGTGGTGCAGCCCAACACCTTATCTGCTTCTGGACACATCTTCCACCTGTG 429
|||||

Db 101 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProVal 120

Qy 430 ATCAACATCATATGGCTCAGAAATAGCAAGTCACTGTCAGTCAAGCGCGGTTTATGAGCCAGC 489
|||||

Db 121 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer 140

Qy 490 TTCCTCGTCAACCGTGACCATCTTCCACAAAGCTGTCTTATCTCACCTTCATCCCTTCT 549
|||||

Db 141 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer 160

Qy 550 GATGATGACATTTATGACTGCAAGTGGAGCACTGGGCGCTGGAGCGCGTTCTGAAA 609
|||||

Db 161 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 180

Qy 610 CACTGGGAACCTGAGATTCCAGCCCCCATGTGTCAGAGCTGACAGAAACT 657
|||||

Db 181 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 196

RESULT 15

S02855

class II histocompatibility antigen RT1-B(b) alpha chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S02855
R:Barran, P.A.; McMaster, W.R.
Immunogenetics 26, 56-62, 1987
A:Title: DNA sequence analysis of the rat RT1-B-alpha gene.
A:Reference number: S02855; MUID:87278361; PMID:3610254
A:Accession: S02855
A:Molecule type: DNA
A:Residues: 1-256 <BAR>
A:Cross-references: UNIPROT:P20037; EMBL:X07550
C:Genetics:
A:Introns: 29/1; 112/1; 206/1
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: class II histocompatibility antigen, RT1-B(b) alpha chain #status pred
F:127-192/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 4.24e-60 Length: 256
Score: 972.00 Matches: 179
Percent Similarity: 89.04% Conservative: 16
Best Local Similarity: 81.74% Mismatches: 24
Query Match: 36.07% Indels: 0
DB: 2 Gaps: 0

US-10-048-116-1 (1-1484) x S02855 (1-256)

Qy 1 ATCCGCTGCAGCAGACTCTGATTTCTGGGGTCTCCGCCCTCAACACACCATCTCAGCCTC 60
|||||

Db 1 MetProLeuSerArgAlaLeuIleLeuGlyValLeuAlaLeuThrThrMetLeuSerPro 20

Qy 61 TGGGAGGTGAAGACGACATTGAGCGGCACAGTAGGCTTCTATGTGTACAACTGTTTAT 120
|||||

Db 21 CysGlyGlyGlnAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyr 40

Qy 121 CAGTCTCTCGACACATTGGCCAGTACACATCAATTTGATGCTGATGATGTTCTCTAT 180
|||||

Db 41 GlnTyrHisGluSerLysGlyGlnTyrThrHisGluPheAspGlyAspGluArgPheTyr 60

Qy 181 GTGACTTGGATGAAGAAAACCTGTCTGGAGGCTTCTCAGTTTGGCCAAATTGATACTC 240
|||||

Db 61 ValAspLeuAspLysLysGluThrIleTrpArgIleProGluPheGlyGlnLeuIleSer 80

Qy 241 TTTGAGCCCCAAGGTGAGCTGCAAAACATAGCTGCAGAAAACACAACTTGGGAATCTTG 300
|||||

Db 81 PheAspProGlnGlyAlaLeuArgAsnIleAlaIleIleLysHisAsnLeuGluIleLeu 100

Qy 301 ACTAAGAGGTCAAAATTTCCGCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTTCCCC 360
|||||

Db 101 MetLysArgSerAsnSerThrProAlaValAsnGluValProGluAlaThrValPheSer 120

Qy 361 AAGTCCCTCTGTCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420
|||||

Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140

Qy 421 CCACCTGTGATCAACATCATCATGGCTCAGAAATAGCAAGTCACTGACAGACGGGTTTAT 480
|||||

Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysProLeuThrGluGlyValTyr 160

Qy 481 GAGACACAGTCTCTCGTCAACCGTACCATTTCTTCCACAAGCTGTCTTATCTCACCTTC 540
|||||

Db 161 GluThrSerPheLeuIleAsnSerAspTyrSerPheHisLysMetAlaTyrLeuThrPhe 180

Qy 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGGACCG 600
|||||

Db 181 IleProSerAsnAspAspIleTyrAspCysLysValGluHisTrpSerLeuAspGluPro 200
|||||

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